SEQUENCE LISTING

<110> Universiteit Leiden
Stichting Binair Vector Systeem
Hooykaas, Paul J.J.
Attikum van, Haico
Bundock, Paul

<120> Nucleic acid integration in eukaryotes

<130> P54997CA00

<140> PCT/NL01/00936
<141> 2003-06-20

<150> EP 00204693.6
<151> 2000-12-22

<150> PCT/NL01/00936
<151> 2001-12-21

<160> 37

<170> PatentIn Ver. 2.1

<210> 1
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (1)..(18)

<400> 1
gggattgctt taaggtag 18

<210> 2
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<220>
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<222> (1)..(18)

<220>
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<400> 2
caaataccct accctacc 18

<210> 3
<211> 21
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<213> Artificial Sequence

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<220>
<221> misc_feature
<222> (1)..(21)

<400> 3
cgtaagattc gccgagtata g 21

<210> 4
<211> 21
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<220>
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<400> 4
cgtttcaaat gggaccacag c 21

<210> 5
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (1)..(19)

<400> 5
agactcacgt ttcgaggcc 19

<210> 6
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (1)..(20)

<400> 6
tcaccgaggc agttccatag 20

<210> 7
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer kanmxp3

<220>
<221> misc_feature

<222> (1)..(22)

<400> 7
tcgcaggtct gcagcgagga gc 22

<210> 8
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (1)..(23)

<400> 8
tcgcctcgac atcatctgcc cag 23

<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
<222> (1)..(22)

<400> 9
tcacatcatg cccctgagct gc 22

<210> 10
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
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fragment derived from a junction sequence

<220>
<221> misc_feature
<222> (1)..(31)
<223> /note="Wherein N stands for any nucleotide
sequence"

<400> 10
caggatatat tcaattgtaa atctcncgag g 31

<210> 11
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
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fragment derived from a junction sequence

<220>
<221> misc_feature
<222> (1)..(37)
<223> /note="Wherein N stands for any nucleotide sequence"

<400> 11
attgtattat atattcaatt gtaaatctcn cgaggta 37

<210> 12
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: part of a PCR fragment derived from a junction sequence

<220>
<221> misc_feature
<222> (1)..(33)
<223> /note="Wherein N stands for any nucleotide sequence"

<400> 12
tgtgggtgtg attcaattgt aaatctcncg agg 33

<210> 13
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: part of a PCR fragment derived from a junction sequence

<220>
<221> misc_feature
<222> (1)..(35)
<223> /note="Wherein N stands for any nucleotide sequence"

<400> 13
gggggcatca gtattcaatt gtaaatctcn cgagg 35

<210> 14
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: part of a PCR fragment derived from a junction sequence

<220>
<221> misc_feature
<222> (1)..(39)

<400> 14

gaggtagatg tgagagagtg tgtgtgggtg tgaagtcga 39

<210> 15
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (1)..(35)
<223> /note="Wherein N stands for any nucleotide sequence"

<400> 15
tctggtagat atattcaatt gtaaatctcn cgagg 35

<210> 16
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
<222> (1)..(35)
<223> /note="Wherein N stands for any nucleotide sequence"

<400> 16
cacatatttc tcattcaatt gtaaatctcn cgagg 35

<210> 17
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
<222> (1)..(35)
<223> /note="Wherein N stands for any nucleotide sequence"

<400> 17
cgactacttt atatccaatt gtaaatctcn cgagg 35

<210> 18
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
<222> (1)..(35)
<223> note="Wherein N stands for any nucleotide sequence"

<400> 18
gaagaaccca ttattcaatt gtaaatctcn cgagg 35

<210> 19
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
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<223> note="Wherein N stands for any nucleotide sequence"

<400> 19
tgggtgtggg ttattcaatt gtaaatctcn cgagg 35

<210> 20
<211> 35
<212> DNA
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<220>
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<222> (1)..(35)
<223> note="Wherein N stands for any nucleotide sequence"

<400> 20
tgggtgtggt gtgttcaatt gtaaatctcn cgagg 35

<210> 21
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: part of a PCR fragment derived from a junction sequence

<220>
<221> misc_feature

<222> (1)..(35)
<223> /note="Wherein N stands for any nucleotide sequence"

<400> 21
tgtgtgggtg tgggtcaatt gtaaatctcn cgagg 35

<210> 22
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: part of a PCR fragment derived from a junction sequence

<220>
<221> misc_feature
<222> (1)..(35)
<223> /note="Wherein N stands for any nucleotide sequence"

<400> 22
cgtcaaggat atattcaatt gtaaatctcn cgagg 35

<210> 23
<211> 602
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> SITE
<222> (1)..(602)
<223> /note="KU 70"

<400> 23
Met Arg Ser Val Thr Asn Ala Phe Gly Asn Ser Gly Glu Leu Asn Asp
1 5 10 15

Gln Val Asp Glu Thr Gly Tyr Arg Lys Phe Asp Ile His Glu Gly Ile
20 25 30

Leu Phe Cys Ile Glu Leu Ser Glu Thr Met Phe Lys Glu Ser Ser Asp
35 40 45

Leu Glu Tyr Lys Ser Pro Leu Leu Glu Ile Leu Glu Ser Leu Asp Glu
50 55 60

Leu Met Ser Gln Leu Val Ile Thr Arg Pro Gly Thr Ala Ile Gly Cys
65 70 75 80

Tyr Phe Tyr Tyr Cys Asn Arg Glu Asp Ala Lys Glu Gly Ile Tyr Glu
85 90 95

Leu Phe Pro Leu Arg Asp Ile Asn Ala Thr Phe Met Lys Lys Leu Asn
100 105 110

Asp Leu Leu Glu Asp Leu Ser Ser Gly Arg Ile Ser Leu Tyr Asp Tyr
115 120 125

Phe Met Phe Gln Gln Thr Gly Ser Glu Lys Gln Val Arg Leu Ser Val
130 135 140

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Leu Phe Thr Phe Met Leu Asp Thr Phe Leu Glu Glu Ile Pro Gly Gln
145                 150                 155                 160

Lys Gln Leu Ser Asn Lys Arg Val Phe Leu Phe Thr Asp Ile Asp Lys
                165                 170                 175

Pro Gln Glu Ala Gln Asp Ile Asp Glu Arg Ala Arg Leu Arg Arg Leu
            180                 185                 190

Thr Ile Asp Leu Phe Asp Asn Lys Val Asn Phe Ala Thr Phe Phe Ile
        195                 200                 205

Gly Tyr Ala Asp Lys Pro Phe Asp Asn Glu Phe Tyr Ser Asp Ile Leu
    210                 215                 220

Gln Leu Gly Ser His Thr Asn Glu Asn Thr Gly Leu Asp Ser Glu Phe
225                 230                 235                 240

Asp Gly Pro Ser Thr Lys Pro Ile Asp Ala Lys Tyr Ile Lys Ser Arg
                245                 250                 255

Ile Leu Arg Lys Lys Glu Val Lys Arg Ile Met Phe Gln Cys Pro Leu
            260                 265                 270

Ile Leu Asp Glu Lys Thr Asn Phe Ile Val Gly Val Lys Gly Tyr Thr
        275                 280                 285

Met Tyr Thr His Glu Lys Ala Gly Val Arg Tyr Lys Leu Val Tyr Glu
    290                 295                 300

His Glu Asp Ile Arg Gln Glu Ala Tyr Ser Lys Arg Lys Phe Leu Asn
305                 310                 315                 320

Pro Ile Thr Gly Glu Asp Val Thr Gly Lys Thr Val Lys Val Tyr Pro
                325                 330                 335

Tyr Gly Asp Leu Asp Ile Asn Leu Ser Asp Ser Gln Asp Gln Ile Val
            340                 345                 350

Met Glu Ala Tyr Thr Gln Lys Asp Ala Phe Leu Lys Ile Ile Gly Phe
        355                 360                 365

Arg Ser Ser Ser Lys Ser Ile His Tyr Phe Asn Asn Ile Asp Lys Ser
    370                 375                 380

Ser Phe Ile Val Pro Asp Glu Ala Lys Tyr Glu Gly Ser Ile Arg Thr
385                 390                 395                 400

Leu Ala Ser Leu Leu Lys Ile Leu Arg Lys Lys Asp Lys Ile Ala Ile
                405                 410                 415

Leu Trp Gly Lys Leu Lys Ser Asn Ser His Pro Ser Leu Tyr Thr Leu
            420                 425                 430

Ser Pro Ser Ser Val Lys Asp Tyr Asn Glu Gly Phe Tyr Leu Tyr Arg
        435                 440                 445

Val Pro Phe Leu Asp Glu Ile Arg Lys Phe Pro Ser Leu Leu Ser Tyr
    450                 455                 460

Asp Asp Gly Ser Glu His Lys Leu Asp Tyr Asp Asn Met Lys Lys Val
465                 470                 475                 480
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Thr Gln Ser Ile Met Gly Tyr Phe Asn Leu Arg Asp Gly Tyr Asn Pro
                485                 490                 495

Ser Asp Phe Lys Asn Pro Leu Leu Gln Lys His Tyr Lys Val Leu His
            500                 505                 510

Asp Tyr Leu Leu Gln Ile Glu Thr Thr Phe Asp Glu Asn Glu Thr Pro
        515                 520                 525

Asn Thr Lys Lys Asp Arg Met Met Arg Glu Asp Asp Ser Leu Arg Lys
    530                 535                 540

Leu Tyr Tyr Ile Arg Asn Lys Ile Leu Glu Ser Glu Lys Ser Glu Asp
545                 550                 555                 560

Pro Ile Ile Gln Arg Leu Asn Lys Tyr Val Lys Ile Trp Asn Met Phe
                565                 570                 575

Tyr Lys Lys Phe Asn Asp Asp Asn Ile Ser Ile Lys Glu Glu Lys Lys
            580                 585                 590

Pro Phe Asp Lys Lys Pro Lys Phe Asn Ile
        595                 600


<210> 24
<211> 609
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)..(609)
<223> /note="KU 70 homologue"

<400> 24
Met Ser Gly Trp Glu Ser Tyr Tyr Lys Thr Glu Gly Asp Glu Glu Ala
  1               5                  10                  15

Glu Glu Glu Gln Glu Glu Asn Leu Glu Ala Ser Gly Asp Tyr Lys Tyr
             20                  25                  30

Ser Gly Arg Asp Ser Leu Ile Phe Leu Val Asp Ala Ser Lys Ala Met
         35                  40                  45

Phe Glu Ser Gln Ser Glu Asp Glu Leu Thr Pro Phe Asp Met Ser Ile
     50                  55                  60

Gln Cys Ile Gln Ser Val Tyr Ile Ser Lys Ile Ile Ser Ser Asp Arg
 65                  70                  75                  80

Asp Leu Leu Ala Val Val Phe Tyr Gly Thr Glu Lys Asp Lys Asn Ser
                 85                  90                  95

Val Asn Phe Lys Asn Ile Tyr Val Leu Gln Glu Leu Asp Asn Pro Gly
            100                 105                 110

Ala Lys Arg Ile Leu Glu Leu Asp Gln Phe Lys Gly Gln Gln Gly Gln
        115                 120                 125

Lys Arg Phe Gln Asp Met Met Gly His Gly Ser Asp Tyr Ser Leu Ser
    130                 135                 140

Glu Val Leu Trp Val Cys Ala Asn Leu Phe Ser Asp Val Gln Phe Lys
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145 150 155 160

Met Ser His Lys Arg Ile Met Leu Phe Thr Asn Glu Asp Asn Pro His
165 170 175

Gly Asn Asp Ser Ala Lys Ala Ser Arg Ala Arg Thr Lys Ala Gly Asp
180 185 190

Leu Arg Asp Thr Gly Ile Phe Leu Asp Leu Met His Leu Lys Lys Pro
195 200 205

Gly Gly Phe Asp Ile Ser Leu Phe Tyr Arg Asp Ile Ile Ser Ile Ala
210 215 220

Glu Asp Glu Asp Leu Arg Val His Phe Glu Glu Ser Ser Lys Leu Glu
225 230 235 240

Asp Leu Leu Arg Lys Val Arg Ala Lys Glu Thr Arg Lys Arg Ala Leu
245 250 255

Ser Arg Leu Lys Leu Lys Leu Asn Lys Asp Ile Val Ile Ser Val Gly
260 265 270

Ile Tyr Asn Leu Val Gln Lys Ala Leu Lys Pro Pro Pro Ile Lys Leu
275 280 285

Tyr Arg Glu Thr Asn Glu Pro Val Lys Thr Lys Thr Arg Thr Phe Asn
290 295 300

Thr Ser Thr Gly Gly Leu Leu Leu Pro Ser Asp Thr Lys Arg Ser Gln
305 310 315 320

Ile Tyr Gly Ser Arg Gln Ile Ile Leu Glu Lys Glu Glu Thr Glu Glu
325 330 335

Leu Lys Arg Phe Asp Asp Pro Gly Leu Met Leu Met Gly Phe Lys Pro
340 345 350

Leu Val Leu Leu Lys Lys His His Tyr Leu Arg Pro Ser Leu Phe Val
355 360 365

Tyr Pro Glu Glu Ser Leu Val Ile Gly Ser Ser Thr Leu Phe Ser Ala
370 375 380

Leu Leu Ile Lys Cys Leu Glu Lys Glu Val Ala Ala Leu Cys Arg Tyr
385 390 395 400

Thr Pro Arg Arg Asn Ile Pro Pro Tyr Phe Val Ala Leu Val Pro Gln
405 410 415

Glu Glu Glu Leu Asp Asp Gln Lys Ile Gln Val Thr Pro Pro Gly Phe
420 425 430

Gln Leu Val Phe Leu Pro Phe Ala Asp Asp Lys Arg Lys Met Pro Phe
435 440 445

Thr Glu Lys Ile Met Ala Thr Pro Glu Gln Val Gly Lys Met Lys Ala
450 455 460

Ile Val Glu Lys Leu Arg Phe Thr Tyr Arg Ser Asp Ser Phe Glu Asn
465 470 475 480

Pro Val Leu Gln Gln His Phe Arg Asn Leu Glu Ala Leu Ala Leu Asp
485 490 495

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Leu Met Glu Pro Glu Gln Ala Val Asp Leu Thr Leu Pro Lys Val Glu
            500                 505                 510

Ala Met Asn Lys Arg Leu Gly Ser Leu Val Asp Glu Phe Lys Glu Leu
        515                 520                 525

Val Tyr Pro Pro Asp Tyr Asn Pro Glu Gly Lys Val Thr Lys Arg Lys
    530                 535                 540

His Asp Asn Glu Gly Ser Gly Ser Lys Arg Pro Lys Val Glu Tyr Ser
545                 550                 555                 560

Glu Glu Glu Leu Lys Thr His Ile Ser Lys Gly Thr Leu Gly Lys Phe
                565                 570                 575

Thr Val Pro Met Leu Lys Glu Ala Cys Arg Ala Tyr Gly Leu Lys Ser
            580                 585                 590

Gly Leu Lys Lys Gln Glu Leu Leu Glu Ala Leu Thr Lys His Phe Gln
        595                 600                 605

Asp
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<210> 25
<211> 477
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> SITE
<222> (1)..(477)
<223> /note="KU 70 homologue"

<400> 25

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Glu Asn Ser Leu Tyr Ser Ala Leu Trp Val Ala Gln Ala Leu Leu Arg
  1               5                  10                  15

Lys Gly Ser Leu Lys Thr Ala Asp Lys Arg Met Phe Leu Phe Thr Asn
             20                  25                  30

Glu Asp Asp Pro Phe Gly Ser Met Arg Ile Ser Val Lys Glu Asp Met
         35                  40                  45

Thr Arg Thr Thr Leu Gln Arg Ala Lys Asp Ala Gln Asp Leu Gly Ile
     50                  55                  60

Ser Ile Glu Leu Leu Pro Leu Ser Gln Pro Asp Lys Gln Phe Asn Ile
 65                  70                  75                  80

Thr Leu Phe Tyr Lys Asp Leu Ile Gly Leu Asn Ser Asp Glu Leu Thr
                 85                  90                  95

Glu Phe Met Pro Ser Val Gly Gln Lys Leu Glu Asp Met Lys Asp Gln
            100                 105                 110

Leu Lys Lys Arg Val Leu Ala Lys Arg Ile Ala Lys Arg Ile Thr Phe
        115                 120                 125

Val Ile Cys Asp Gly Leu Ser Ile Glu Leu Asn Gly Tyr Ala Leu Leu
    130                 135                 140
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Arg Pro Ala Ile Pro Gly Ser Ile Thr Trp Leu Asp Ser Thr Thr Asn
145                 150                 155                 160

Leu Pro Val Lys Val Glu Arg Ser Tyr Ile Cys Thr Asp Thr Gly Ala
                165                 170                 175

Ile Met Gln Asp Pro Ile Gln Arg Ile Gln Pro Tyr Lys Asn Gln Asn
            180                 185                 190

Ile Met Phe Thr Val Glu Glu Leu Ser Gln Val Lys Arg Ile Ser Thr
        195                 200                 205

Gly His Leu Arg Leu Leu Gly Phe Lys Pro Leu Ser Cys Leu Lys Asp
    210                 215                 220

Tyr His Asn Leu Lys Pro Ser Thr Phe Leu Tyr Pro Ser Asp Lys Glu
225                 230                 235                 240

Val Ile Gly Ser Thr Arg Ala Phe Ile Ala Leu His Arg Ser Met Ile
                245                 250                 255

Gln Leu Glu Arg Phe Ala Val Ala Phe Tyr Gly Gly Thr Thr Pro Pro
            260                 265                 270

Arg Leu Val Ala Leu Val Ala Gln Asp Glu Ile Glu Ser Asp Gly Gly
        275                 280                 285

Gln Val Glu Pro Pro Gly Ile Asn Met Ile Tyr Leu Pro Tyr Ala Asn
    290                 295                 300

Asp Ile Arg Asp Ile Asp Glu Leu His Ser Lys Pro Gly Val Ala Xaa
305                 310                 315                 320

Pro Arg Ala Ser Asp Asp Gln Leu Lys Lys Ala Ser Ala Leu Met Arg
                325                 330                 335

Arg Leu Glu Leu Lys Asp Phe Ser Val Cys Gln Phe Ala Asn Pro Ala
            340                 345                 350

Leu Gln Arg His Tyr Ala Ile Leu Gln Ala Ile Ala Leu Asp Glu Asn
        355                 360                 365

Glu Leu Arg Glu Thr Arg Asp Glu Thr Leu Pro Asp Glu Glu Gly Met
    370                 375                 380

Asn Arg Pro Ala Val Val Lys Ala Ile Glu Gln Phe Lys Gln Ser Ile
385                 390                 395                 400

Tyr Gly Asp Asp Pro Asp Glu Glu Ser Asp Ser Gly Ala Lys Glu Lys
                405                 410                 415

Ser Lys Lys Arg Lys Ala Gly Asp Ala Asp Asp Gly Lys Tyr Asp Tyr
            420                 425                 430

Ile Glu Leu Ala Lys Thr Gly Lys Leu Lys Asp Leu Thr Val Val Glu
        435                 440                 445

Leu Lys Thr Tyr Leu Thr Ala Asn Asn Leu Leu Val Ser Gly Lys Lys
    450                 455                 460

Glu Val Leu Ile Asn Arg Ile Leu Thr His Ile Gly Lys
465                 470                 475
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<210> 26
<211> 944
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> SITE
<222> (1)..(944)
<223> /note="LIG 4"

<400> 26
Met Ile Ser Ala Leu Asp Ser Ile Pro Glu Pro Gln Asn Phe Ala Pro
1 5 10 15

Ser Pro Asp Phe Lys Trp Leu Cys Glu Glu Leu Phe Val Lys Ile His
20 25 30

Glu Val Gln Ile Asn Gly Thr Ala Gly Thr Gly Lys Ser Arg Ser Phe
35 40 45

Lys Tyr Tyr Glu Ile Ile Ser Asn Phe Val Glu Met Trp Arg Lys Thr
50 55 60

Val Gly Asn Asn Ile Tyr Pro Ala Leu Val Leu Ala Leu Pro Tyr Arg
65 70 75 80

Asp Arg Arg Ile Tyr Asn Ile Lys Asp Tyr Val Leu Ile Arg Thr Ile
85 90 95

Cys Ser Tyr Leu Lys Leu Pro Lys Asn Ser Ala Thr Glu Gln Arg Leu
100 105 110

Lys Asp Trp Lys Gln Arg Val Gly Lys Gly Gly Asn Leu Ser Ser Leu
115 120 125

Leu Val Glu Glu Ile Ala Lys Arg Arg Ala Glu Pro Ser Ser Lys Ala
130 135 140

Ile Thr Ile Asp Asn Val Asn His Tyr Leu Asp Ser Leu Ser Gly Asp
145 150 155 160

Arg Phe Ala Ser Gly Arg Gly Phe Lys Ser Leu Val Lys Ser Lys Pro
165 170 175

Phe Leu His Cys Val Glu Asn Met Ser Phe Val Glu Leu Lys Tyr Phe
180 185 190

Phe Asp Ile Val Leu Lys Asn Arg Val Ile Gly Gly Gln Glu His Lys
195 200 205

Leu Leu Asn Cys Trp His Pro Asp Ala Gln Asp Tyr Leu Ser Val Ile
210 215 220

Ser Asp Leu Lys Val Val Thr Ser Lys Leu Tyr Asp Pro Lys Val Arg
225 230 235 240

Leu Lys Asp Asp Asp Leu Ser Ile Lys Val Gly Phe Ala Phe Ala Pro
245 250 255

Gln Leu Ala Lys Lys Val Asn Leu Ser Tyr Glu Lys Ile Cys Arg Thr
260 265 270

Leu His Asp Asp Phe Leu Val Glu Glu Lys Met Asp Gly Glu Arg Ile
275 280 285

Gln Val His Tyr Met Asn Tyr Gly Glu Ser Ile Lys Phe Phe Ser Arg
290 295 300

Arg Gly Ile Asp Tyr Thr Tyr Leu Tyr Gly Ala Ser Leu Ser Ser Gly
305 310 315 320

Thr Ile Ser Gln His Leu Arg Phe Thr Asp Ser Val Lys Glu Cys Val
325 330 335

Leu Asp Gly Glu Met Val Thr Phe Asp Ala Lys Arg Arg Val Ile Leu
340 345 350

Pro Phe Gly Leu Val Lys Gly Ser Ala Lys Glu Ala Leu Ser Phe Asn
355 360 365

Ser Ile Asn Asn Val Asp Phe His Pro Leu Tyr Met Val Phe Asp Leu
370 375 380

Leu Tyr Leu Asn Gly Thr Ser Leu Thr Pro Leu Pro Leu His Gln Arg
385 390 395 400

Lys Gln Tyr Leu Asn Ser Ile Leu Ser Pro Leu Lys Asn Ile Val Glu
405 410 415

Ile Val Arg Ser Ser Arg Cys Tyr Gly Val Glu Ser Ile Lys Lys Ser
420 425 430

Leu Glu Val Ala Ile Ser Leu Gly Ser Glu Gly Val Val Leu Lys Tyr
435 440 445

Tyr Asn Ser Ser Tyr Asn Val Ala Ser Arg Asn Asn Asn Trp Ile Lys
450 455 460

Val Lys Pro Glu Tyr Leu Glu Glu Phe Gly Glu Asn Leu Asp Leu Ile
465 470 475 480

Val Ile Gly Arg Asp Ser Gly Lys Lys Asp Ser Phe Met Leu Gly Leu
485 490 495

Leu Val Leu Asp Glu Glu Glu Tyr Lys Lys His Gln Gly Asp Ser Ser
500 505 510

Glu Ile Val Asp His Ser Ser Gln Glu Lys His Ile Gln Asn Ser Arg
515 520 525

Arg Arg Val Lys Lys Ile Leu Ser Phe Cys Ser Ile Ala Asn Gly Ile
530 535 540

Ser Gln Glu Glu Phe Lys Glu Ile Asp Arg Lys Thr Arg Gly His Trp
545 550 555 560

Lys Arg Thr Ser Glu Val Ala Pro Pro Ala Ser Ile Leu Glu Phe Gly
565 570 575

Ser Lys Ile Pro Ala Glu Trp Ile Asp Pro Ser Glu Ser Ile Val Leu
580 585 590

Glu Ile Lys Ser Arg Ser Leu Asp Asn Thr Glu Thr Asn Met Gln Lys
595 600 605

Tyr Ala Thr Asn Cys Thr Leu Tyr Gly Gly Tyr Cys Lys Arg Ile Arg
610 615 620

Tyr Asp Lys Glu Trp Thr Asp Cys Tyr Thr Leu Asn Asp Leu Tyr Glu
625 630 635 640

Ser Arg Thr Val Lys Ser Asn Pro Ser Tyr Gln Ala Glu Arg Ser Gln
645 650 655

Leu Gly Leu Ile Arg Lys Lys Arg Lys Arg Val Leu Ile Ser Asp Ser
660 665 670

Phe His Gln Asn Arg Lys Gln Leu Pro Ile Ser Asn Ile Phe Ala Gly
675 680 685

Leu Leu Phe Tyr Val Leu Ser Asp Tyr Val Thr Glu Asp Thr Gly Ile
690 695 700

Arg Ile Thr Arg Ala Glu Leu Glu Lys Thr Ile Val Glu His Gly Gly
705 710 715 720

Lys Leu Ile Tyr Asn Val Ile Leu Lys Arg His Ser Ile Gly Asp Val
725 730 735

Arg Leu Ile Ser Cys Lys Thr Thr Thr Glu Cys Lys Ala Leu Ile Asp
740 745 750

Arg Gly Tyr Asp Ile Leu His Pro Asn Trp Val Leu Asp Cys Ile Ala
755 760 765

Tyr Lys Arg Leu Ile Leu Ile Glu Pro Asn Tyr Cys Phe Asn Val Ser
770 775 780

Gln Lys Met Arg Ala Val Ala Glu Lys Arg Val Asp Cys Leu Gly Asp
785 790 795 800

Ser Phe Glu Asn Asp Ile Ser Glu Thr Lys Leu Ser Ser Leu Tyr Lys
805 810 815

Ser Gln Leu Ser Leu Pro Pro Met Gly Glu Leu Glu Ile Asp Ser Glu
820 825 830

Val Arg Arg Phe Pro Leu Phe Leu Phe Ser Asn Arg Ile Ala Tyr Val
835 840 845

Pro Arg Arg Lys Ile Ser Thr Glu Asp Asp Ile Ile Glu Met Lys Ile
850 855 860

Lys Leu Phe Gly Gly Lys Ile Thr Asp Gln Gln Ser Leu Cys Asn Leu
865 870 875 880

Ile Ile Ile Pro Tyr Thr Asp Pro Ile Leu Arg Lys Asp Cys Met Asn
885 890 895

Glu Val His Glu Lys Ile Lys Glu Gln Ile Lys Ala Ser Asp Thr Ile
900 905 910

Pro Lys Ile Ala Arg Val Val Ala Pro Glu Trp Val Asp His Ser Ile
915 920 925

Asn Glu Asn Cys Gln Val Pro Glu Glu Asp Phe Pro Val Val Asn Tyr
930 935 940

<210> 27
<211> 844
<212> PRT

<213> Homo sapiens

<220>
<221> SITE
<222> (1)..(844)
<223> /note="LIG 4 homologue"

<400> 27
Met Arg Leu Ile Leu Pro Gln Leu Glu Arg Glu Arg Met Ala Tyr Gly
1 5 10 15

Ile Lys Glu Thr Met Leu Ala Lys Leu Tyr Ile Glu Leu Leu Asn Leu
20 25 30

Pro Arg Asp Gly Lys Asp Ala Leu Lys Leu Leu Asn Tyr Arg Thr Pro
35 40 45

Thr Gly Thr His Gly Asp Ala Gly Asp Phe Ala Met Ile Ala Tyr Phe
50 55 60

Val Leu Lys Pro Arg Cys Leu Gln Lys Gly Ser Leu Thr Ile Gln Gln
65 70 75 80

Val Asn Asp Leu Leu Asp Ser Ile Ala Ser Asn Asn Ser Ala Lys Arg
85 90 95

Lys Asp Leu Ile Lys Lys Ser Leu Leu Gln Leu Ile Thr Gln Ser Ser
100 105 110

Ala Leu Glu Gln Lys Trp Leu Ile Arg Met Ile Ile Lys Asp Leu Lys
115 120 125

Leu Gly Val Ser Gln Gln Thr Ile Phe Ser Val Phe His Asn Asp Ala
130 135 140

Ala Glu Leu His Asn Val Thr Thr Asp Leu Glu Lys Val Cys Arg Gln
145 150 155 160

Leu His Asp Pro Ser Val Gly Leu Ser Asp Ile Ser Ile Thr Leu Phe
165 170 175

Ser Ala Ser Lys Pro Met Leu Ala Ala Ile Ala Asp Ile Glu His Ile
180 185 190

Glu Lys Asp Met Lys His Gln Ser Phe Tyr Ile Glu Thr Lys Leu Asp
195 200 205

Gly Glu Arg Met Gln Met His Lys Asp Gly Asp Val Tyr Lys Tyr Phe
210 215 220

Ser Arg Asn Gly Tyr Asn Tyr Thr Asp Gln Phe Gly Ala Ser Pro Thr
225 230 235 240

Glu Gly Ser Leu Thr Pro Phe Ile His Asn Ala Phe Lys Ala Asp Ile
245 250 255

Gln Ile Cys Ile Leu Asp Gly Glu Met Met Ala Tyr Asn Pro Asn Thr
260 265 270

Gln Thr Phe Met Gln Lys Gly Thr Lys Phe Asp Ile Lys Arg Met Val
275 280 285

Glu Asp Ser Asp Leu Gln Thr Cys Tyr Cys Val Phe Asp Val Leu Met
290 295 300

Val Asn Asn Lys Lys Leu Gly His Glu Thr Leu Arg Lys Arg Tyr Glu
305 310 315 320

Ile Leu Ser Ser Ile Phe Thr Pro Ile Pro Gly Arg Ile Glu Ile Val
325 330 335

Gln Lys Thr Gln Ala His Thr Lys Asn Glu Val Ile Asp Ala Leu Asn
340 345 350

Glu Ala Ile Asp Lys Arg Glu Glu Gly Ile Met Val Lys Gln Pro Leu
355 360 365

Ser Ile Tyr Lys Pro Asp Lys Arg Gly Glu Gly Trp Leu Lys Ile Lys
370 375 380

Pro Glu Tyr Val Ser Gly Leu Met Asp Glu Leu Asp Ile Leu Ile Val
385 390 395 400

Gly Gly Tyr Trp Gly Lys Gly Ser Arg Gly Gly Met Met Ser His Phe
405 410 415

Leu Cys Ala Val Ala Glu Lys Pro Pro Pro Gly Glu Lys Pro Ser Val
420 425 430

Phe His Thr Leu Ser Arg Val Gly Ser Gly Cys Thr Met Lys Glu Leu
435 440 445

Tyr Asp Leu Gly Leu Lys Leu Ala Lys Tyr Trp Lys Pro Phe His Arg
450 455 460

Lys Ala Pro Pro Ser Ser Ile Leu Cys Gly Thr Glu Lys Pro Glu Val
465 470 475 480

Tyr Ile Glu Pro Cys Asn Ser Val Ile Val Gln Ile Lys Ala Ala Glu
485 490 495

Ile Val Pro Ser Asp Met Tyr Lys Thr Gly Cys Thr Leu Arg Phe Pro
500 505 510

Arg Ile Glu Lys Ile Arg Asp Asp Lys Glu Trp His Glu Cys Met Thr
515 520 525

Leu Asp Asp Leu Glu Gln Leu Arg Gly Lys Ala Ser Gly Lys Leu Ala
530 535 540

Ser Lys His Leu Tyr Ile Gly Gly Asp Asp Glu Pro Gln Glu Lys Lys
545 550 555 560

Arg Lys Ala Ala Pro Lys Met Lys Lys Val Ile Gly Ile Ile Glu His
565 570 575

Leu Lys Ala Pro Asn Leu Thr Asn Val Asn Lys Ile Ser Asn Ile Phe
580 585 590

Glu Asp Val Glu Phe Cys Val Met Ser Gly Thr Asp Ser Gln Pro Lys
595 600 605

Pro Asp Leu Glu Asn Arg Ile Ala Glu Phe Gly Gly Tyr Ile Val Gln
610 615 620

Asn Pro Gly Pro Asp Thr Tyr Cys Val Ile Ala Gly Ser Glu Asn Ile
625 630 635 640

```
Arg Val Lys Asn Ile Ile Leu Ser Asn Lys His Asp Val Val Lys Pro
                645                 650                 655

Ala Trp Leu Leu Glu Cys Phe Lys Thr Lys Ser Phe Val Pro Trp Gln
            660                 665                 670

Pro Arg Phe Met Ile His Met Cys Pro Ser Thr Lys Glu His Phe Ala
        675                 680                 685

Arg Glu Tyr Asp Cys Tyr Gly Asp Ser Tyr Phe Ile Asp Thr Asp Leu
    690                 695                 700

Asn Gln Leu Lys Glu Val Phe Ser Gly Ile Lys Asn Ser Asn Glu Gln
705                 710                 715                 720

Thr Pro Glu Glu Met Ala Ser Leu Ile Ala Asp Leu Glu Tyr Arg Tyr
                725                 730                 735

Ser Trp Asp Cys Ser Pro Leu Ser Met Phe Arg Arg His Thr Val Tyr
            740                 745                 750

Leu Asp Ser Tyr Ala Val Ile Asn Asp Leu Ser Thr Lys Asn Glu Gly
        755                 760                 765

Thr Arg Leu Ala Ile Lys Ala Leu Glu Leu Arg Phe His Gly Ala Lys
    770                 775                 780

Val Val Ser Cys Leu Ala Glu Gly Val Ser His Val Ile Ile Gly Glu
785                 790                 795                 800

Asp His Ser Arg Val Ala Asp Phe Lys Ala Phe Arg Arg Thr Phe Lys
                805                 810                 815

Arg Lys Phe Lys Ile Leu Lys Glu Ser Trp Val Thr Asp Ser Ile Asp
            820                 825                 830

Lys Cys Glu Leu Gln Glu Glu Asn Gln Tyr Leu Ile
        835                 840
```

<210> 28
<211> 1219
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> SITE
<222> (1)..(1219)
<223> /note="LIG 4 homologue"

<400> 28

```
Met Thr Glu Glu Ile Lys Phe Ser Val Leu Val Ser Leu Phe Asn Trp
  1               5                  10                  15

Ile Gln Lys Ser Lys Thr Ser Ser Gln Lys Arg Ser Lys Phe Arg Lys
             20                  25                  30

Phe Leu Asp Thr Tyr Cys Lys Pro Ser Asp Tyr Phe Val Ala Val Arg
         35                  40                  45

Leu Ile Ile Pro Ser Leu Asp Arg Glu Arg Gly Ser Tyr Gly Leu Lys
     50                  55                  60

Glu Ser Val Leu Ala Thr Cys Leu Ile Asp Ala Leu Gly Ile Ser Arg
```

```
 65                  70                  75                  80

Asp Ala Pro Asp Ala Val Arg Leu Leu Asn Trp Arg Lys Gly Gly Thr
                85                  90                  95

Ala Lys Ala Gly Ala Asn Ala Gly Asn Phe Ser Leu Ile Ala Ala Glu
            100                 105                 110

Val Leu Gln Arg Arg Gln Gly Met Ala Ser Gly Gly Leu Thr Ile Lys
        115                 120                 125

Glu Leu Asn Asp Leu Leu Asp Arg Leu Ala Ser Ser Glu Asn Arg Ala
    130                 135                 140

Glu Lys Thr Leu Val Leu Ser Thr Leu Ile Gln Lys Thr Asn Ala Gln
145                 150                 155                 160

Glu Met Lys Trp Val Ile Arg Ile Ile Leu Lys Asp Leu Lys Leu Gly
                165                 170                 175

Met Ser Glu Lys Ser Ile Phe Gln Glu Phe His Pro Asp Ala Glu Asp
            180                 185                 190

Leu Phe Asn Val Thr Cys Asp Leu Lys Leu Val Cys Glu Lys Leu Arg
        195                 200                 205

Asp Arg His Gln Arg His Lys Arg Gln Asp Ile Glu Val Gly Lys Ala
    210                 215                 220

Val Arg Pro Gln Leu Ala Met Arg Ile Gly Asp Val Asn Ala Ala Trp
225                 230                 235                 240

Lys Lys Leu His Gly Lys Asp Val Val Ala Glu Cys Lys Phe Asp Gly
                245                 250                 255

Asp Arg Ile Gln Ile His Lys Asn Gly Thr Asp Ile His Tyr Phe Ser
            260                 265                 270

Arg Asn Phe Leu Asp His Ser Glu Tyr Ala His Ala Met Ser Asp Leu
        275                 280                 285

Ile Val Gln Asn Ile Leu Val Asp Lys Cys Ile Leu Asp Gly Glu Met
    290                 295                 300

Leu Val Trp Asp Thr Ser Leu Asn Arg Phe Ala Glu Phe Gly Ser Asn
305                 310                 315                 320

Gln Glu Ile Ala Lys Ala Ala Arg Glu Gly Leu Asp Ser His Lys Gln
                325                 330                 335

Leu Cys Tyr Val Ala Phe Asp Val Leu Tyr Val Gly Asp Thr Ser Val
            340                 345                 350

Ile His Gln Ser Leu Lys Glu Arg His Glu Leu Leu Lys Lys Val Val
        355                 360                 365

Lys Pro Leu Lys Gly Arg Leu Glu Val Leu Val Pro Glu Gly Gly Leu
    370                 375                 380

Asn Val His Arg Pro Ser Gly Glu Pro Ser Trp Ser Ile Val Val His
385                 390                 395                 400

Ala Ala Ala Asp Val Glu Arg Phe Phe Lys Glu Thr Val Glu Asn Arg
                405                 410                 415
```

Asp Glu Gly Ile Val Leu Lys Asp Leu Glu Ser Lys Trp Glu Pro Gly
420 425 430

Asp Arg Ser Gly Lys Trp Met Lys Leu Lys Pro Glu Tyr Ile Arg Ala
435 440 445

Gly Ala Asp Leu Asp Val Leu Ile Ile Gly Gly Tyr Tyr Gly Ser Gly
450 455 460

Arg Arg Gly Gly Glu Val Ala Gln Phe Leu Val Ala Leu Ala Asp Arg
465 470 475 480

Ala Glu Ala Asn Val Tyr Pro Arg Arg Phe Met Ser Phe Cys Arg Val
485 490 495

Gly Thr Gly Leu Ser Asp Asp Glu Leu Asn Thr Val Val Ser Lys Leu
500 505 510

Lys Pro Tyr Phe Arg Lys Asn Glu His Pro Lys Lys Ala Pro Pro Ser
515 520 525

Phe Tyr Gln Val Thr Asn His Ser Lys Glu Arg Pro Asp Val Trp Ile
530 535 540

Asp Ser Pro Glu Lys Ser Ile Ile Leu Ser Ile Thr Ser Asp Ile Arg
545 550 555 560

Thr Ile Arg Ser Glu Val Phe Val Ala Pro Tyr Ser Leu Arg Phe Pro
565 570 575

Arg Ile Asp Lys Val Arg Tyr Asp Lys Pro Trp His Glu Cys Leu Asp
580 585 590

Val Gln Ala Phe Val Glu Leu Val Asn Ser Ser Asn Gly Thr Thr Gln
595 600 605

Lys Gln Lys Glu Ser Glu Ser Thr Gln Asp Asn Pro Lys Val Asn Lys
610 615 620

Ser Ser Lys Arg Gly Glu Lys Lys Asn Val Ser Leu Val Pro Ser Gln
625 630 635 640

Phe Ile Gln Thr Asp Val Ser Asp Ile Lys Gly Lys Thr Ser Ile Phe
645 650 655

Ser Asn Met Ile Phe Tyr Phe Val Asn Val Pro Arg Ser His Ser Leu
660 665 670

Glu Thr Phe His Lys Met Val Val Glu Asn Gly Gly Lys Phe Ser Met
675 680 685

Asn Leu Asn Asn Ser Val Thr His Cys Ile Ala Ala Glu Ser Ser Gly
690 695 700

Ile Lys Tyr Gln Ala Ala Lys Arg Gln Arg Asp Val Ile His Phe Ser
705 710 715 720

Trp Val Leu Asp Cys Cys Ser Arg Asn Lys Met Leu Pro Leu Leu Pro
725 730 735

Lys Tyr Phe Leu His Leu Thr Asp Ala Ser Arg Thr Lys Leu Gln Asp
740 745 750

```
Asp Ile Asp Glu Phe Ser Asp Ser Tyr Tyr Trp Asp Leu Asp Leu Glu
        755                 760                 765

Gly Leu Lys Gln Val Leu Ser Asn Ala Lys Gln Ser Glu Asp Ser Lys
    770                 775                 780

Ser Ile Asp Tyr Tyr Lys Lys Lys Leu Cys Pro Glu Lys Arg Trp Ser
785                 790                 795                 800

Cys Leu Leu Ser Cys Cys Val Tyr Phe Tyr Pro Tyr Ser Gln Thr Leu
                805                 810                 815

Ser Thr Glu Glu Glu Ala Leu Leu Gly Ile Met Ala Lys Arg Leu Met
            820                 825                 830

Leu Glu Val Leu Met Ala Gly Gly Lys Val Ser Asn Asn Leu Ala His
        835                 840                 845

Ala Ser His Leu Val Val Leu Ala Met Ala Glu Glu Pro Leu Asp Phe
    850                 855                 860

Thr Leu Val Ser Lys Ser Phe Ser Glu Met Glu Lys Arg Leu Leu Leu
865                 870                 875                 880

Lys Lys Arg Leu His Val Val Ser Ser His Trp Leu Glu Glu Ser Leu
                885                 890                 895

Gln Arg Glu Glu Lys Leu Cys Glu Asp Val Tyr Thr Leu Arg Pro Lys
            900                 905                 910

Tyr Met Glu Glu Ser Asp Thr Glu Glu Ser Asp Lys Ser Glu His Asp
        915                 920                 925

Thr Thr Glu Val Ala Ser Gln Gly Ser Ala Gln Thr Lys Glu Pro Ala
    930                 935                 940

Ser Ser Lys Ile Ala Ile Thr Ser Ser Arg Gly Arg Ser Asn Thr Arg
945                 950                 955                 960

Ala Val Lys Arg Gly Arg Ser Ser Thr Asn Ser Leu Gln Arg Val Gln
                965                 970                 975

Arg Arg Arg Gly Lys Gln Pro Ser Lys Ile Ser Gly Asp Glu Thr Glu
            980                 985                 990

Glu Ser Asp Ala Ser Glu Glu Lys Val Ser Thr Arg Leu Ser Asp Ile
        995                1000                1005

Ala Glu Glu Thr Asp Ser Phe Gly Glu Ala Gln Arg Asn Ser Ser Arg
   1010                1015                1020

Gly Lys Cys Ala Lys Arg Gly Lys Ser Arg Val Gly Gln Thr Gln Arg
1025                1030                1035                1040

Val Gln Arg Ser Arg Arg Gly Lys Lys Ala Ala Lys Ile Gly Gly Asp
                1045                1050                1055

Glu Ser Asp Glu Asn Asp Glu Leu Asp Gly Asn Asn Asn Val Ser Ala
            1060                1065                1070

Asp Ala Glu Glu Gly Asn Ala Ala Gly Arg Ser Val Glu Asn Glu Glu
        1075                1080                1085

Thr Arg Glu Pro Asp Ile Ala Lys Tyr Thr Glu Ser Gln Gln Arg Asp
```

```
   1090                1095                1100

Asn Thr Val Ala Val Glu Glu Ala Leu Gln Asp Ser Arg Asn Ala Lys
1105                1110                1115                1120

Thr Glu Met Asp Met Lys Glu Lys Leu Gln Ile His Glu Asp Pro Leu
                1125                1130                1135

Gln Ala Met Leu Met Lys Met Phe Pro Ile Pro Ser Gln Lys Thr Thr
            1140                1145                1150

Glu Thr Ser Asn Arg Thr Thr Gly Glu Tyr Arg Lys Ala Asn Val Ser
        1155                1160                1165

Gly Glu Cys Glu Ser Ser Glu Lys Arg Lys Leu Asp Ala Glu Thr Asp
    1170                1175                1180

Asn Thr Ser Val Asn Ala Gly Ala Glu Ser Asp Val Val Pro Pro Leu
1185                1190                1195                1200

Val Lys Lys Lys Lys Val Ser Tyr Arg Asp Val Ala Gly Glu Leu Leu
                1205                1210                1215

Lys Asp Trp
```

<210> 29
<211> 692
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> SITE
<222> (1)..(692)
<223> /note="MRE 11"

<400> 29

```
Met Asp Tyr Pro Asp Pro Asp Thr Ile Arg Ile Leu Ile Thr Thr Asp
  1               5                  10                  15

Asn His Val Gly Tyr Asn Glu Asn Asp Pro Ile Thr Gly Asp Asp Ser
            20                  25                  30

Trp Lys Thr Phe His Glu Val Met Met Leu Ala Lys Asn Asn Asn Val
        35                  40                  45

Asp Met Val Val Gln Ser Gly Asp Leu Phe His Val Asn Lys Pro Ser
    50                  55                  60

Lys Lys Ser Leu Tyr Gln Val Leu Lys Thr Leu Arg Leu Cys Cys Met
65                  70                  75                  80

Gly Asp Lys Pro Cys Glu Leu Glu Leu Leu Ser Asp Pro Ser Gln Val
                85                  90                  95

Phe His Tyr Asp Glu Phe Thr Asn Val Asn Tyr Glu Asp Pro Asn Phe
            100                 105                 110

Asn Ile Ser Ile Pro Val Phe Gly Ile Ser Gly Asn His Asp Asp Ala
        115                 120                 125

Ser Gly Asp Ser Leu Leu Cys Pro Met Asp Ile Leu His Ala Thr Gly
    130                 135                 140
```

Leu Ile Asn His Phe Gly Lys Val Ile Glu Ser Asp Lys Ile Lys Val
145 150 155 160

Val Pro Leu Leu Phe Gln Lys Gly Ser Thr Lys Leu Ala Leu Tyr Gly
165 170 175

Leu Ala Ala Val Arg Asp Glu Arg Leu Phe Arg Thr Phe Lys Asp Gly
180 185 190

Gly Val Thr Phe Glu Val Pro Thr Met Arg Glu Gly Glu Trp Phe Asn
195 200 205

Leu Met Cys Val His Gln Asn His Thr Gly His Thr Asn Thr Ala Phe
210 215 220

Leu Pro Glu Gln Phe Leu Pro Asp Phe Leu Asp Met Val Ile Trp Gly
225 230 235 240

His Glu His Glu Cys Ile Pro Asn Leu Val His Asn Pro Ile Lys Asn
245 250 255

Phe Asp Val Leu Gln Pro Gly Ser Ser Val Ala Thr Ser Leu Cys Glu
260 265 270

Ala Glu Ala Gln Pro Lys Tyr Val Phe Ile Leu Asp Ile Lys Tyr Gly
275 280 285

Glu Ala Pro Lys Met Thr Pro Ile Pro Leu Glu Thr Ile Arg Thr Phe
290 295 300

Lys Met Lys Ser Ile Ser Leu Gln Asp Val Pro His Leu Arg Pro His
305 310 315 320

Asp Lys Asp Ala Thr Ser Lys Tyr Leu Ile Glu Gln Val Glu Glu Met
325 330 335

Ile Arg Asp Ala Asn Glu Glu Thr Lys Gln Lys Leu Ala Asp Asp Gly
340 345 350

Glu Gly Asp Met Val Ala Glu Leu Pro Lys Pro Leu Ile Arg Leu Arg
355 360 365

Val Asp Tyr Ser Ala Pro Ser Asn Thr Gln Ser Pro Ile Asp Tyr Gln
370 375 380

Val Glu Asn Pro Arg Arg Phe Ser Asn Arg Phe Val Gly Arg Val Ala
385 390 395 400

Asn Gly Asn Asn Val Val Gln Phe Tyr Lys Lys Arg Ser Pro Val Thr
405 410 415

Arg Ser Lys Lys Ser Gly Ile Asn Gly Thr Ser Ile Ser Asp Arg Asp
420 425 430

Val Glu Lys Leu Phe Ser Glu Ser Gly Gly Glu Leu Glu Val Gln Thr
435 440 445

Leu Val Asn Asp Leu Leu Asn Lys Met Gln Leu Ser Leu Leu Pro Glu
450 455 460

Val Gly Leu Asn Glu Ala Val Lys Lys Phe Val Asp Lys Asp Glu Lys
465 470 475 480

```
Thr Ala Leu Lys Glu Phe Ile Ser His Glu Ile Ser Asn Glu Val Gly
                485                 490                 495

Ile Leu Ser Thr Asn Glu Glu Phe Leu Arg Thr Asp Asp Ala Glu Glu
            500                 505                 510

Met Lys Ala Leu Ile Lys Gln Val Lys Arg Ala Asn Ser Val Arg Pro
        515                 520                 525

Thr Pro Pro Lys Glu Asn Asp Glu Thr Asn Phe Ala Phe Asn Gly Asn
    530                 535                 540

Gly Leu Asp Ser Phe Arg Ser Ser Asn Arg Glu Val Arg Thr Gly Ser
545                 550                 555                 560

Pro Asp Ile Thr Gln Ser His Val Asp Asn Glu Ser Arg Ile Thr His
                565                 570                 575

Ile Ser Gln Ala Glu Ser Ser Lys Pro Thr Ser Lys Pro Lys Arg Val
            580                 585                 590

Arg Thr Ala Thr Lys Lys Lys Ile Pro Ala Phe Ser Asp Ser Thr Val
        595                 600                 605

Ile Ser Asp Ala Glu Asn Glu Leu Gly Asp Asn Asn Asp Ala Gln Asp
    610                 615                 620

Asp Val Asp Ile Asp Glu Asn Asp Ile Ile Met Val Ser Thr Asp Glu
625                 630                 635                 640

Glu Asp Ala Ser Tyr Gly Leu Leu Asn Gly Arg Lys Thr Lys Thr Lys
                645                 650                 655

Thr Arg Pro Ala Ala Ser Thr Lys Thr Ala Ser Arg Arg Gly Lys Gly
            660                 665                 670

Arg Ala Ser Arg Thr Pro Lys Thr Asp Ile Leu Gly Ser Leu Leu Ala
        675                 680                 685

Lys Lys Arg Lys
    690


<210> 30
<211> 708
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)..(708)
<223> /note="MRE 11 homologue"

<400> 30
Met Ser Thr Ala Asp Ala Leu Asp Asp Glu Asn Thr Phe Lys Ile Leu
  1               5                  10                  15

Val Ala Thr Asp Ile His Leu Gly Phe Met Glu Lys Asp Ala Ala Arg
             20                  25                  30

Gly Asn Asp Thr Phe Val Thr Leu Asp Glu Ile Leu Arg Leu Ala Gln
         35                  40                  45

Glu Asn Glu Val Asp Phe Ile Leu Leu Gly Gly Asp Leu Phe His Glu
```

```
     50                  55                  60

Asn Lys Pro Ser Arg Lys Thr Leu His Thr Cys Leu Glu Leu Leu Arg
 65                  70                  75                  80

Lys Tyr Cys Met Gly Asp Arg Pro Val Gln Phe Glu Ile Leu Ser Asp
                 85                  90                  95

Gln Ser Val Asn Phe Gly Phe Ser Lys Phe Pro Trp Val Asn Tyr Gln
            100                 105                 110

Asp Gly Asn Leu Asn Ile Ser Ile Pro Val Phe Ser Ile His Gly Asn
        115                 120                 125

His Asp Asp Pro Thr Gly Ala Asp Ala Leu Cys Ala Leu Asp Ile Leu
    130                 135                 140

Ser Cys Ala Gly Phe Val Asn His Phe Gly Arg Ser Met Ser Val Glu
145                 150                 155                 160

Lys Ile Asp Ile Ser Pro Val Leu Leu Gln Lys Gly Ser Thr Lys Ile
                165                 170                 175

Ala Leu Tyr Gly Leu Gly Ser Ile Pro Asp Glu Arg Leu Tyr Arg Met
            180                 185                 190

Phe Val Asn Lys Lys Val Thr Met Leu Arg Pro Lys Glu Asp Glu Asn
        195                 200                 205

Ser Trp Phe Asn Leu Phe Val Ile His Gln Asn Arg Ser Lys His Gly
    210                 215                 220

Ser Thr Asn Phe Ile Pro Glu Gln Phe Leu Asp Asp Phe Ile Asp Leu
225                 230                 235                 240

Val Ile Trp Gly His Glu His Glu Cys Lys Ile Ala Pro Thr Lys Asn
                245                 250                 255

Glu Gln Gln Leu Phe Tyr Ile Ser Gln Pro Gly Ser Ser Val Val Thr
            260                 265                 270

Ser Leu Ser Pro Gly Glu Ala Val Lys Lys His Val Gly Leu Leu Arg
        275                 280                 285

Ile Lys Gly Arg Lys Met Asn Met His Lys Ile Pro Leu His Thr Val
    290                 295                 300

Arg Gln Phe Phe Met Glu Asp Ile Val Leu Ala Asn His Pro Asp Ile
305                 310                 315                 320

Phe Asn Pro Asp Asn Pro Lys Val Thr Gln Ala Ile Gln Ser Phe Cys
                325                 330                 335

Leu Glu Lys Ile Glu Glu Met Leu Glu Asn Ala Glu Arg Glu Arg Leu
            340                 345                 350

Gly Asn Ser His Gln Pro Glu Lys Pro Leu Val Arg Leu Arg Val Asp
        355                 360                 365

Tyr Ser Gly Gly Phe Glu Pro Phe Ser Val Leu Arg Phe Ser Gln Lys
    370                 375                 380

Phe Val Asp Arg Val Ala Asn Pro Lys Asp Ile Ile His Phe Phe Arg
385                 390                 395                 400
```

```
His Arg Glu Gln Lys Glu Lys Thr Gly Glu Glu Ile Asn Phe Gly Lys
                405                 410                 415

Leu Ile Thr Lys Pro Ser Glu Gly Thr Thr Leu Arg Val Glu Asp Leu
            420                 425                 430

Val Lys Gln Tyr Phe Gln Thr Ala Glu Lys Asn Val Gln Leu Ser Leu
        435                 440                 445

Leu Thr Glu Arg Gly Met Gly Glu Ala Val Gln Glu Phe Val Asp Lys
    450                 455                 460

Glu Glu Lys Asp Ala Ile Glu Glu Leu Val Lys Tyr Gln Leu Glu Lys
465                 470                 475                 480

Thr Gln Arg Phe Leu Lys Glu Arg His Ile Asp Ala Leu Glu Asp Lys
                485                 490                 495

Ile Asp Glu Glu Val Arg Arg Phe Arg Glu Thr Arg Gln Lys Asn Thr
            500                 505                 510

Asn Glu Glu Asp Asp Glu Val Arg Glu Ala Met Thr Arg Ala Arg Ala
        515                 520                 525

Leu Arg Ser Gln Ser Glu Glu Ser Ala Ser Ala Phe Ser Ala Asp Asp
    530                 535                 540

Leu Met Ser Ile Asp Leu Ala Glu Gln Met Ala Asn Asp Ser Asp Asp
545                 550                 555                 560

Ser Ile Ser Ala Ala Thr Asn Lys Gly Arg Gly Arg Gly Arg Gly Arg
                565                 570                 575

Arg Gly Gly Arg Gly Gln Asn Ser Ala Ser Arg Gly Gly Ser Gln Arg
            580                 585                 590

Gly Arg Ala Phe Lys Ser Thr Arg Gln Gln Pro Ser Arg Asn Val Thr
        595                 600                 605

Thr Lys Asn Tyr Ser Glu Val Ile Glu Val Asp Glu Ser Asp Val Glu
    610                 615                 620

Glu Asp Ile Phe Pro Thr Thr Ser Lys Thr Asp Gln Arg Trp Ser Ser
625                 630                 635                 640

Thr Ser Ser Ser Lys Ile Met Ser Gln Ser Gln Val Ser Lys Gly Val
                645                 650                 655

Asp Phe Glu Ser Ser Glu Asp Asp Asp Asp Asp Pro Phe Met Asn Thr
            660                 665                 670

Ser Ser Leu Arg Arg Asn Arg Arg Leu Ile Tyr Leu Leu Ala Leu Arg
        675                 680                 685

Asn Met Gln Asp Thr Gly Lys Met Lys Cys Tyr Lys Leu Arg Val Tyr
    690                 695                 700

Ser Leu Arg Phe
705
```

<210> 31
<211> 720

<212> PRT
<213> Arabidopsis thaliana

<220>
<221> SITE
<222> (1)..(720)
<223> /note="MRE 11 homologue"

<400> 31
Met Ser Arg Glu Asp Phe Ser Asp Thr Leu Arg Val Leu Val Ala Thr
1 5 10 15

Asp Cys His Leu Gly Tyr Met Glu Lys Asp Glu Ile Arg Arg His Asp
20 25 30

Ser Phe Lys Ala Phe Glu Glu Ile Cys Ser Ile Ala Glu Glu Lys Gln
35 40 45

Val Asp Phe Leu Leu Leu Gly Gly Asp Leu Phe His Glu Asn Lys Pro
50 55 60

Ser Arg Thr Thr Leu Val Lys Ala Ile Glu Ile Leu Arg Arg His Cys
65 70 75 80

Leu Asn Asp Lys Pro Val Gln Phe Gln Val Val Ser Asp Gln Thr Val
85 90 95

Asn Phe Gln Asn Ala Phe Gly Gln Val Asn Tyr Glu Asp Pro His Phe
100 105 110

Asn Val Gly Leu Pro Val Phe Ser Ile His Gly Asn His Asp Asp Pro
115 120 125

Ala Gly Val Asp Asn Leu Ser Ala Ile Asp Ile Leu Ser Ala Cys Asn
130 135 140

Leu Val Asn Tyr Phe Gly Lys Met Val Leu Gly Gly Ser Gly Val Gly
145 150 155 160

Gln Ile Thr Leu Tyr Pro Ile Leu Met Lys Lys Gly Ser Thr Thr Val
165 170 175

Ala Leu Tyr Gly Leu Gly Asn Ile Arg Asp Glu Arg Leu Asn Arg Met
180 185 190

Phe Gln Thr Pro His Ala Val Gln Trp Met Arg Pro Glu Val Gln Glu
195 200 205

Gly Cys Asp Val Ser Asp Trp Phe Asn Ile Leu Val Leu His Gln Asn
210 215 220

Arg Val Lys Ser Asn Pro Lys Asn Ala Ile Ser Glu His Phe Leu Pro
225 230 235 240

Arg Phe Leu Asp Phe Ile Val Trp Gly His Glu His Glu Cys Leu Ile
245 250 255

Asp Pro Gln Glu Val Ser Gly Met Gly Phe His Ile Thr Gln Pro Gly
260 265 270

Ser Ser Val Ala Thr Ser Leu Ile Asp Gly Glu Ser Lys Pro Lys His
275 280 285

Val Leu Leu Leu Glu Ile Lys Gly Asn Gln Tyr Arg Pro Thr Lys Ile

```
    290                 295                 300

Pro Leu Thr Ser Val Arg Pro Phe Glu Tyr Thr Glu Ile Val Leu Lys
305                 310                 315                 320

Asp Glu Ser Asp Ile Asp Pro Asn Asp Gln Asn Ser Ile Leu Glu His
                325                 330                 335

Leu Asp Lys Val Val Arg Asn Leu Ile Glu Lys Ala Ser Lys Lys Ala
            340                 345                 350

Val Asn Arg Ser Glu Ile Lys Leu Pro Leu Val Arg Ile Lys Val Asp
        355                 360                 365

Tyr Ser Gly Phe Met Thr Ile Asn Pro Gln Arg Phe Gly Gln Lys Tyr
    370                 375                 380

Val Gly Lys Val Ala Asn Pro Gln Asp Ile Leu Ile Phe Ser Lys Ala
385                 390                 395                 400

Ser Lys Lys Gly Arg Ser Glu Ala Asn Ile Asp Asp Ser Glu Arg Leu
                405                 410                 415

Arg Pro Glu Glu Leu Asn Gln Gln Asn Ile Glu Ala Leu Val Ala Glu
            420                 425                 430

Ser Asn Leu Lys Met Glu Ile Leu Pro Val Asn Asp Leu Asp Val Ala
        435                 440                 445

Leu His Asn Phe Val Asn Lys Asp Asp Lys Leu Ala Phe Tyr Ser Cys
    450                 455                 460

Val Gln Tyr Asn Leu Gln Glu Thr Arg Gly Lys Leu Ala Lys Asp Ser
465                 470                 475                 480

Asp Ala Lys Lys Phe Glu Glu Asp Asp Leu Ile Leu Lys Val Gly Glu
                485                 490                 495

Cys Leu Glu Glu Arg Leu Lys Asp Arg Ser Thr Arg Pro Thr Gly Ser
            500                 505                 510

Ser Gln Phe Leu Ser Thr Gly Leu Thr Ser Glu Asn Leu Thr Lys Gly
        515                 520                 525

Ser Ser Gly Ile Ala Asn Ala Ser Phe Ser Asp Asp Glu Asp Thr Thr
    530                 535                 540

Gln Met Ser Gly Leu Ala Pro Pro Thr Arg Gly Arg Arg Gly Ser Ser
545                 550                 555                 560

Thr Ala Asn Thr Thr Arg Gly Arg Ala Lys Ala Pro Thr Arg Gly Arg
                565                 570                 575

Gly Arg Gly Lys Ala Ser Ser Ala Met Lys Gln Thr Thr Leu Asp Ser
            580                 585                 590

Ser Leu Gly Phe Arg Gln Ser Gln Arg Ser Ala Ser Ala Ala Ala Ser
        595                 600                 605

Ala Ala Phe Lys Ser Ala Ser Thr Ile Gly Glu Asp Asp Val Asp Ser
    610                 615                 620

Pro Ser Ser Glu Glu Val Glu Pro Glu Asp Phe Asn Lys Pro Asp Ser
625                 630                 635                 640
```

```
Ser Ser Glu Asp Asp Glu Ser Thr Lys Gly Lys Gly Arg Lys Arg Pro
                645                 650                 655

Ala Thr Thr Lys Arg Gly Arg Gly Arg Gly Ser Gly Thr Ser Lys Arg
            660                 665                 670

Gly Arg Lys Asn Glu Ser Ser Ser Ser Leu Asn Arg Leu Leu Ser Ser
        675                 680                 685

Lys Asp Asp Asp Glu Asp Glu Asp Asp Glu Asp Arg Glu Lys Lys Leu
    690                 695                 700

Asn Lys Ser Gln Pro Arg Val Thr Arg Asn Tyr Gly Ala Leu Arg Arg
705                 710                 715                 720


<210> 32
<211> 1312
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> SITE
<222> (1)..(1312)
<223> /note="RAD 50"

<400> 32
Met Ser Ala Ile Tyr Lys Leu Ser Ile Gln Gly Ile Arg Ser Phe Asp
  1               5                  10                  15

Ser Asn Asp Arg Glu Thr Ile Glu Phe Gly Lys Pro Leu Thr Leu Ile
             20                  25                  30

Val Gly Met Asn Gly Ser Gly Lys Thr Thr Ile Ile Glu Cys Leu Lys
         35                  40                  45

Tyr Ala Thr Thr Gly Asp Leu Pro Pro Asn Ser Lys Gly Gly Val Phe
     50                  55                  60

Ile His Asp Pro Lys Ile Thr Gly Glu Lys Asp Ile Arg Ala Gln Val
 65                  70                  75                  80

Lys Leu Ala Phe Thr Ser Ala Asn Gly Leu Asn Met Ile Val Thr Arg
                85                  90                  95

Asn Ile Gln Leu Leu Met Lys Lys Thr Thr Thr Thr Phe Lys Thr Leu
            100                 105                 110

Glu Gly Gln Leu Val Ala Ile Asn Asn Ser Gly Asp Arg Ser Thr Leu
        115                 120                 125

Ser Thr Arg Ser Leu Glu Leu Asp Ala Gln Val Pro Leu Tyr Leu Gly
    130                 135                 140

Val Pro Lys Ala Ile Leu Glu Tyr Val Ile Phe Cys His Gln Glu Asp
145                 150                 155                 160

Ser Leu Trp Pro Leu Ser Glu Pro Ser Asn Leu Lys Lys Lys Phe Asp
                165                 170                 175

Glu Ile Phe Gln Ala Met Lys Phe Thr Lys Ala Leu Asp Asn Leu Lys
            180                 185                 190
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Ser Ile Lys Lys Asp Met Ser Val Asp Ile Lys Leu Leu Lys Gln Ser
195 200 205

Val Glu His Leu Lys Leu Asp Lys Asp Arg Ser Lys Ala Met Lys Leu
210 215 220

Asn Ile His Gln Leu Gln Thr Lys Ile Asp Gln Tyr Asn Glu Glu Val
225 230 235 240

Ser Glu Ile Glu Ser Gln Leu Asn Glu Ile Thr Glu Lys Ser Asp Lys
245 250 255

Leu Phe Lys Ser Asn Gln Asp Phe Gln Lys Ile Leu Ser Lys Val Glu
260 265 270

Asn Leu Lys Asn Thr Lys Leu Ser Ile Ser Asp Gln Val Lys Arg Leu
275 280 285

Ser Asn Ser Ile Asp Ile Leu Asp Leu Ser Lys Pro Asp Leu Gln Asn
290 295 300

Leu Leu Ala Asn Phe Ser Lys Val Leu Met Asp Lys Asn Asn Gln Leu
305 310 315 320

Arg Asp Leu Glu Thr Asp Ile Ser Ser Leu Lys Asp Arg Gln Ser Ser
325 330 335

Leu Gln Ser Leu Ser Asn Ser Leu Ile Arg Arg Gln Gly Glu Leu Glu
340 345 350

Ala Gly Lys Glu Thr Tyr Glu Lys Asn Arg Asn His Leu Ser Ser Leu
355 360 365

Lys Glu Ala Phe Gln His Lys Phe Gln Gly Leu Ser Asn Ile Glu Asn
370 375 380

Ser Asp Met Ala Gln Val Asn His Glu Met Ser Gln Phe Lys Ala Phe
385 390 395 400

Ile Ser Gln Asp Leu Thr Asp Thr Ile Asp Gln Phe Ala Lys Asp Ile
405 410 415

Gln Leu Lys Glu Thr Asn Leu Ser Asp Leu Ile Lys Ser Ile Thr Val
420 425 430

Asp Ser Gln Asn Leu Glu Tyr Asn Lys Lys Asp Arg Ser Lys Leu Ile
435 440 445

His Asp Ser Glu Glu Leu Ala Glu Lys Leu Lys Ser Phe Lys Ser Leu
450 455 460

Ser Thr Gln Asp Ser Leu Asn His Glu Leu Glu Asn Leu Lys Thr Tyr
465 470 475 480

Lys Glu Lys Leu Gln Ser Trp Glu Ser Glu Asn Ile Ile Pro Lys Leu
485 490 495

Asn Gln Lys Ile Glu Glu Lys Asn Asn Glu Met Ile Ile Leu Glu Asn
500 505 510

Gln Ile Glu Lys Phe Gln Asp Arg Ile Met Lys Thr Asn Gln Gln Ala
515 520 525

Asp Leu Tyr Ala Lys Leu Gly Leu Ile Lys Lys Ser Ile Asn Thr Lys

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    530                 535                 540

Leu Asp Glu Leu Gln Lys Ile Thr Glu Lys Leu Gln Asn Asp Ser Arg
545                 550                 555                 560

Ile Arg Gln Val Phe Pro Leu Thr Gln Glu Phe Gln Arg Ala Asp Leu
                565                 570                 575

Glu Met Asp Phe Gln Lys Leu Phe Ile Asn Met Gln Lys Asn Ile Ala
            580                 585                 590

Ile Asn Asn Lys Lys Met His Glu Leu Asp Arg Arg Tyr Thr Asn Ala
        595                 600                 605

Leu Tyr Asn Leu Asn Thr Ile Glu Lys Asp Leu Gln Asp Asn Gln Lys
    610                 615                 620

Ser Lys Glu Lys Val Ile Gln Leu Leu Ser Glu Asn Leu Pro Glu Asp
625                 630                 635                 640

Cys Thr Ile Asp Glu Tyr Asn Asp Val Leu Glu Glu Thr Glu Leu Ser
                645                 650                 655

Tyr Lys Thr Ala Leu Glu Asn Leu Lys Met His Gln Thr Thr Leu Glu
            660                 665                 670

Phe Asn Arg Lys Ala Leu Glu Ile Ala Glu Arg Asp Ser Cys Cys Tyr
        675                 680                 685

Leu Cys Ser Arg Lys Phe Glu Asn Glu Ser Phe Lys Ser Lys Leu Leu
    690                 695                 700

Gln Glu Leu Lys Thr Lys Thr Asp Ala Asn Phe Glu Lys Thr Leu Lys
705                 710                 715                 720

Asp Thr Val Gln Asn Glu Lys Glu Tyr Leu His Ser Leu Arg Leu Leu
                725                 730                 735

Glu Lys His Ile Ile Thr Leu Asn Ser Ile Asn Glu Lys Ile Asp Asn
            740                 745                 750

Ser Gln Lys Cys Leu Glu Lys Ala Lys Glu Glu Thr Lys Thr Ser Lys
        755                 760                 765

Ser Lys Leu Asp Glu Leu Glu Val Asp Ser Thr Lys Leu Lys Asp Glu
    770                 775                 780

Lys Glu Leu Ala Glu Ser Glu Ile Arg Pro Leu Ile Glu Lys Phe Thr
785                 790                 795                 800

Tyr Leu Glu Lys Glu Leu Lys Asp Leu Glu Asn Ser Ser Lys Thr Ile
                805                 810                 815

Ser Glu Glu Leu Ser Ile Tyr Asn Thr Ser Glu Asp Gly Ile Gln Thr
            820                 825                 830

Val Asp Glu Leu Arg Asp Gln Gln Arg Lys Met Asn Asp Ser Leu Arg
        835                 840                 845

Glu Leu Arg Lys Thr Ile Ser Asp Leu Gln Met Glu Lys Asp Glu Lys
    850                 855                 860

Val Arg Glu Asn Ser Arg Met Ile Asn Leu Ile Lys Glu Lys Glu Leu
865                 870                 875                 880
```

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Thr Val Ser Glu Ile Glu Ser Ser Leu Thr Gln Lys Gln Asn Ile Asp
                885                 890                 895

Asp Ser Ile Arg Ser Lys Arg Glu Asn Ile Asn Asp Ile Asp Ser Arg
            900                 905                 910

Val Lys Glu Leu Glu Ala Arg Ile Ile Ser Leu Lys Asn Lys Lys Asp
        915                 920                 925

Glu Ala Gln Ser Val Leu Asp Lys Val Lys Asn Glu Arg Asp Ile Gln
    930                 935                 940

Val Arg Asn Lys Gln Lys Thr Val Ala Asp Ile Asn Arg Leu Ile Asp
945                 950                 955                 960

Arg Phe Gln Thr Ile Tyr Asn Glu Val Val Asp Phe Glu Ala Lys Gly
                965                 970                 975

Phe Asp Glu Leu Gln Thr Thr Ile Lys Glu Leu Glu Leu Asn Lys Ala
            980                 985                 990

Gln Met Leu Glu Leu Lys Glu Gln Leu Asp Leu Lys Ser Asn Glu Val
        995                1000                1005

Asn Glu Glu Lys Arg Lys Leu Ala Asp Ser Asn Asn Glu Glu Lys Asn
   1010                1015                1020

Leu Lys Gln Asn Leu Glu Leu Ile Glu Leu Lys Ser Gln Leu Gln His
1025                1030                1035                1040

Ile Glu Ser Glu Ile Ser Arg Leu Asp Val Gln Asn Ala Glu Ala Glu
                1045                1050                1055

Arg Asp Lys Tyr Gln Glu Glu Ser Leu Arg Leu Arg Thr Arg Phe Glu
            1060                1065                1070

Lys Leu Ser Ser Glu Asn Ala Gly Lys Leu Gly Glu Met Lys Gln Leu
        1075                1080                1085

Gln Asn Gln Ile Asp Ser Leu Thr His Gln Leu Arg Thr Asp Tyr Lys
   1090                1095                1100

Asp Ile Glu Lys Asn Tyr His Lys Glu Trp Val Glu Leu Gln Thr Arg
1105                1110                1115                1120

Ser Phe Val Thr Asp Asp Ile Asp Val Tyr Ser Lys Ala Leu Asp Ser
                1125                1130                1135

Ala Ile Met Lys Tyr His Gly Leu Lys Met Gln Asp Ile Asn Arg Ile
            1140                1145                1150

Ile Asp Glu Leu Trp Lys Arg Thr Tyr Ser Gly Thr Asp Ile Asp Thr
        1155                1160                1165

Ile Lys Ile Arg Ser Asp Glu Val Ser Ser Thr Val Lys Gly Lys Ser
   1170                1175                1180

Tyr Asn Tyr Arg Val Val Met Tyr Lys Gln Asp Val Glu Leu Asp Met
1185                1190                1195                1200

Arg Gly Arg Cys Ser Ala Gly Gln Lys Val Leu Ala Ser Ile Ile Ile
                1205                1210                1215
```

```
Arg Leu Ala Leu Ser Glu Thr Phe Gly Ala Asn Cys Gly Val Ile Ala
          1220                1225                1230

Leu Asp Glu Pro Thr Thr Asn Leu Asp Glu Glu Asn Ile Glu Ser Leu
       1235                1240                1245

Ala Lys Ser Leu His Asn Ile Ile Asn Met Arg Arg His Gln Lys Asn
   1250                1255                1260

Phe Gln Leu Ile Val Ile Thr His Asp Glu Lys Phe Leu Gly His Met
1265                1270                1275                1280

Asn Ala Ala Ala Phe Thr Asp His Phe Phe Lys Val Lys Arg Asp Asp
               1285                1290                1295

Arg Gln Lys Ser Gln Ile Glu Trp Val Asp Ile Asn Arg Val Thr Tyr
          1300                1305                1310


<210> 33
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<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)..(1318)
<223> /note="RAD 50 homologue"

<400> 33
Met Leu Ile Phe Ser Val Arg Asp Met Phe Ala Lys Met Ser Ile Leu
  1               5                  10                  15

Gly Val Arg Ser Phe Gly Ile Glu Asp Lys Asp Lys Gln Ile Ile Thr
             20                  25                  30

Phe Phe Ser Pro Leu Thr Ile Leu Val Gly Pro Asn Gly Ala Gly Lys
         35                  40                  45

Thr Thr Ile Ile Glu Cys Leu Lys Tyr Ile Cys Thr Gly Asp Phe Pro
     50                  55                  60

Pro Gly Thr Lys Gly Asn Thr Phe Val His Asp Pro Lys Val Ala Gln
 65                  70                  75                  80

Glu Thr Asp Val Arg Ala Gln Ile Arg Leu Gln Phe Arg Asp Val Asn
                 85                  90                  95

Gly Glu Leu Ile Ala Val Gln Arg Ser Met Val Cys Thr Gln Lys Ser
            100                 105                 110

Lys Lys Thr Glu Phe Lys Thr Leu Glu Gly Val Ile Thr Arg Thr Lys
        115                 120                 125

His Gly Glu Lys Val Ser Leu Ser Ser Lys Cys Ala Glu Ile Asp Arg
    130                 135                 140

Glu Met Ile Ser Ser Leu Gly Val Ser Lys Ala Val Leu Asn Asn Val
145                 150                 155                 160

Ile Phe Cys His Gln Glu Asp Ser Asn Trp Pro Leu Ser Glu Gly Lys
                165                 170                 175

Ala Leu Lys Gln Lys Phe Asp Glu Ile Phe Ser Ala Thr Arg Tyr Ile
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            180                 185                 190

Lys Ala Leu Glu Thr Leu Arg Gln Val Arg Gln Thr Gln Gly Gln Lys
        195                 200                 205

Val Glu Glu Tyr Gln Met Glu Leu Lys Tyr Leu Lys Gln Tyr Lys Glu
    210                 215                 220

Lys Ala Cys Glu Ile Arg Asp Gln Ile Thr Ser Lys Glu Ala Gln Leu
225                 230                 235                 240

Thr Ser Ser Lys Glu Ile Val Lys Ser Tyr Glu Asn Glu Leu Asp Pro
                245                 250                 255

Leu Lys Asn Arg Leu Lys Glu Ile Glu His Asn Leu Ser Lys Ile Met
            260                 265                 270

Lys Leu Asp Asn Glu Ile Lys Ala Leu Asp Ser Arg Lys Lys Gln Met
        275                 280                 285

Glu Lys Asp Asn Ser Glu Leu Glu Glu Lys Met Glu Lys Val Phe Gln
    290                 295                 300

Gly Thr Asp Glu Gln Leu Asn Asp Leu Tyr His Asn His Gln Arg Thr
305                 310                 315                 320

Val Arg Glu Lys Glu Arg Lys Leu Val Asp Cys His Arg Glu Leu Glu
                325                 330                 335

Lys Leu Asn Lys Glu Ser Arg Leu Leu Asn Gln Glu Lys Ser Glu Leu
            340                 345                 350

Leu Val Glu Gln Gly Arg Leu Gln Leu Gln Ala Asp Arg His Gln Glu
        355                 360                 365

His Ile Arg Ala Arg Asp Ser Leu Ile Gln Ser Leu Ala Thr Gln Leu
    370                 375                 380

Glu Leu Asp Gly Phe Glu Arg Gly Pro Phe Ser Glu Arg Gln Ile Lys
385                 390                 395                 400

Asn Phe His Lys Leu Val Arg Glu Arg Gln Glu Gly Glu Ala Lys Thr
                405                 410                 415

Ala Asn Gln Leu Met Asn Asp Phe Ala Glu Lys Glu Thr Leu Lys Gln
            420                 425                 430

Lys Gln Ile Asp Glu Ile Arg Asp Lys Lys Thr Gly Leu Gly Arg Ile
        435                 440                 445

Ile Glu Leu Lys Ser Glu Ile Leu Ser Lys Lys Gln Asn Glu Leu Lys
    450                 455                 460

Asn Val Lys Tyr Glu Leu Gln Gln Leu Glu Gly Ser Ser Asp Arg Ile
465                 470                 475                 480

Leu Glu Leu Asp Gln Glu Leu Ile Lys Ala Glu Arg Glu Leu Ser Lys
                485                 490                 495

Ala Glu Lys Asn Ser Asn Val Glu Thr Leu Lys Met Glu Val Ile Ser
            500                 505                 510

Leu Gln Asn Glu Lys Ala Asp Leu Asp Arg Thr Leu Arg Lys Leu Asp
        515                 520                 525
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Gln Glu Met Glu Gln Leu Asn His His Thr Thr Thr Arg Thr Gln Met
530 535 540

Glu Met Leu Thr Lys Asp Lys Ala Asp Lys Asp Glu Gln Ile Arg Lys
545 550 555 560

Ile Lys Ser Arg His Ser Asp Glu Leu Thr Ser Leu Leu Gly Tyr Phe
565 570 575

Pro Asn Lys Lys Gln Leu Glu Asp Trp Leu His Ser Lys Ser Lys Glu
580 585 590

Ile Asn Gln Thr Arg Asp Arg Leu Ala Lys Leu Asn Lys Glu Leu Ala
595 600 605

Ser Ser Glu Gln Asn Lys Asn His Ile Asn Asn Glu Leu Glu Arg Lys
610 615 620

Glu Glu Gln Leu Ser Ser Tyr Glu Asp Lys Leu Phe Asp Val Cys Gly
625 630 635 640

Ser Gln Asp Phe Glu Ser Asp Leu Asp Arg Leu Lys Glu Glu Ile Glu
645 650 655

Lys Ser Ser Lys Gln Arg Ala Met Leu Ala Gly Ala Thr Ala Val Tyr
660 665 670

Ser Gln Phe Ile Thr Gln Leu Thr Asp Glu Asn Gln Ser Cys Cys Pro
675 680 685

Val Cys Gln Arg Val Phe Gln Thr Glu Ala Glu Leu Gln Glu Ala Ile
690 695 700

Ser Asp Leu Gln Ser Lys Leu Arg Leu Ala Pro Asp Lys Leu Lys Ser
705 710 715 720

Thr Glu Ser Glu Leu Lys Lys Lys Glu Lys Arg Arg Asp Glu Met Leu
725 730 735

Gly Leu Ala Pro Met Arg Gln Ser Ile Ile Asp Leu Lys Glu Lys Glu
740 745 750

Ile Pro Glu Leu Arg Asn Lys Leu Gln Asn Val Asn Arg Asp Ile Gln
755 760 765

Arg Leu Lys Asn Asp Ile Glu Glu Gln Glu Thr Leu Leu Gly Thr Ile
770 775 780

Met Pro Glu Glu Glu Ser Ala Lys Val Cys Leu Thr Asp Val Thr Ile
785 790 795 800

Met Glu Arg Phe Gln Met Glu Leu Lys Asp Val Glu Arg Lys Ile Ala
805 810 815

Gln Gln Ala Ala Lys Leu Gln Gly Ile Asp Leu Asp Arg Thr Val Gln
820 825 830

Gln Val Asn Gln Glu Lys Gln Glu Lys Gln His Lys Leu Asp Thr Val
835 840 845

Ser Ser Lys Ile Glu Leu Asn Arg Lys Leu Ile Gln Asp Gln Gln Glu
850 855 860

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Gln Ile Gln His Leu Lys Ser Thr Thr Asn Glu Leu Lys Ser Glu Lys
865                 870                 875                 880

Leu Gln Ile Ser Thr Asn Leu Gln Arg Arg Gln Gln Leu Glu Glu Gln
                885                 890                 895

Thr Val Glu Leu Ser Thr Glu Val Gln Ser Leu Tyr Arg Glu Ile Lys
            900                 905                 910

Asp Ala Lys Glu Gln Val Ser Pro Leu Glu Thr Thr Leu Glu Lys Phe
        915                 920                 925

Gln Gln Glu Lys Glu Glu Leu Ile Asn Lys Lys Asn Thr Ser Asn Lys
    930                 935                 940

Ile Ala Gln Asp Lys Leu Asn Asp Ile Lys Glu Lys Val Lys Asn Ile
945                 950                 955                 960

His Gly Tyr Met Lys Asp Ile Glu Asn His Ile Gln Asp Gly Lys Asp
                965                 970                 975

Asp Tyr Met Lys Gln Lys Glu Thr Glu Leu Asn Lys Val Ile Ala Gln
            980                 985                 990

Leu Ser Glu Cys Glu Lys His Lys Glu Lys Ile Asn Glu Asp Met Arg
        995                1000                1005

Leu Met Arg Gln Asp Ile Asp Thr Gln Lys Ile Gln Glu Arg Trp Leu
   1010                1015                1020

Gln Asp Asn Leu Thr Leu Arg Lys Arg Asn Glu Glu Leu Lys Glu Val
1025                1030                1035                1040

Glu Glu Glu Gly Lys Gln His Leu Lys Glu Met Gly Gln Met Gln Val
                1045                1050                1055

Leu Gln Met Lys Ser Glu His Gln Lys Leu Glu Glu Asn Ile Asp Asn
            1060                1065                1070

Ile Lys Arg Asn His Asn Leu Ala Leu Gly Arg Gln Lys Gly Tyr Glu
        1075                1080                1085

Glu Glu Ile Ile His Phe Lys Lys Glu Leu Arg Glu Pro Gln Phe Arg
   1090                1095                1100

Asp Ala Glu Glu Lys Tyr Arg Glu Met Met Ile Val Met Arg Thr Thr
1105                1110                1115                1120

Glu Leu Val Asn Lys Asp Leu Asp Ile Tyr Tyr Lys Thr Leu Asp Gln
                1125                1130                1135

Ala Ile Met Lys Phe His Ser Met Lys Met Glu Glu Ile Asn Lys Ile
            1140                1145                1150

Ile Arg Asp Leu Trp Arg Ser Thr Tyr Arg Gly Gln Asp Ile Glu Tyr
        1155                1160                1165

Ile Glu Ile Arg Ser Asp Ala Asp Glu Asn Val Ser Ala Ser Asp Lys
   1170                1175                1180

Arg Arg Asn Tyr Asn Tyr Arg Val Val Met Leu Lys Gly Asp Thr Ala
1185                1190                1195                1200

Leu Asp Met Arg Gly Arg Cys Ser Ala Gly Gln Lys Val Leu Ala Ser
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                1205                1210                1215

Leu Ile Ile Arg Leu Ala Leu Ala Glu Thr Phe Cys Leu Asn Cys Gly
            1220                1225                1230

Ile Ile Ala Leu Asp Glu Pro Thr Thr Asn Leu Asp Arg Glu Asn Ile
        1235                1240                1245

Glu Ser Leu Ala His Ala Leu Val Glu Ile Ile Lys Ser Arg Ser Gln
    1250                1255                1260

Gln Arg Asn Phe Gln Leu Leu Val Ile Thr His Asp Glu Asp Phe Val
1265                1270                1275                1280

Glu Leu Leu Gly Arg Ser Glu Tyr Val Glu Lys Phe Tyr Arg Ile Lys
                1285                1290                1295

Lys Asn Ile Asp Gln Cys Ser Glu Ile Val Lys Cys Ser Val Ser Ser
            1300                1305                1310

Leu Gly Phe Asn Val His
        1315


<210> 34
<211> 1292
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> SITE
<222> (1)..(1292)
<223> /note="RAD 50 homologue"

<400> 34
Met Ser Thr Val Asp Lys Met Leu Ile Lys Gly Ile Arg Ser Phe Asp
  1               5                  10                  15

Pro Glu Asn Lys Asn Val Val Thr Phe Phe Arg Pro Leu Thr Leu Ile
             20                  25                  30

Val Gly Ala Asn Gly Ala Gly Lys Thr Thr Ile Ile Glu Cys Leu Lys
         35                  40                  45

Val Ser Cys Thr Gly Glu Leu Pro Pro Asn Ala Arg Ser Gly His Ser
     50                  55                  60

Phe Ile His Asp Pro Lys Val Ala Gly Glu Thr Glu Thr Lys Ala Gln
 65                  70                  75                  80

Ile Lys Leu Arg Phe Lys Thr Ala Ala Gly Lys Asp Val Val Cys Ile
                 85                  90                  95

Arg Ser Phe Gln Leu Thr Gln Lys Ala Ser Lys Met Glu Tyr Lys Ala
            100                 105                 110

Ile Glu Ser Val Leu Gln Thr Ile Asn Pro His Thr Gly Glu Lys Val
        115                 120                 125

Cys Leu Ser Tyr Arg Cys Ala Asp Met Asp Arg Glu Ile Pro Ala Leu
    130                 135                 140

Met Gly Val Ser Lys Ala Ile Leu Glu Asn Val Ile Phe Val His Gln
145                 150                 155                 160
```

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Asp Glu Ser Asn Trp Pro Leu Gln Asp Pro Ser Thr Leu Lys Lys Lys
                165                 170                 175

Phe Asp Asp Ile Phe Ser Ala Thr Arg Tyr Thr Lys Ala Leu Glu Val
            180                 185                 190

Ile Lys Lys Leu His Lys Asp Gln Ala Gln Glu Ile Lys Thr Phe Lys
        195                 200                 205

Leu Lys Leu Glu Asn Leu Gln Thr Leu Lys Asp Ala Ala Tyr Lys Leu
    210                 215                 220

Arg Glu Ser Ile Ala Gln Asp Gln Glu Arg Thr Glu Ser Ser Lys Val
225                 230                 235                 240

Gln Met Leu Glu Leu Glu Thr Ser Val Gln Lys Val Asp Ala Glu Val
                245                 250                 255

His Asn Lys Glu Met Met Leu Lys Asp Leu Arg Lys Leu Gln Asp Gln
            260                 265                 270

Val Ser Ile Lys Thr Ala Glu Arg Ser Thr Leu Phe Lys Glu Gln Gln
        275                 280                 285

Arg Gln Tyr Ala Ala Leu Pro Glu Glu Asn Glu Asp Thr Ile Glu Glu
    290                 295                 300

Leu Lys Glu Trp Lys Ser Lys Phe Glu Glu Arg Leu Ala Leu Leu Gly
305                 310                 315                 320

Thr Lys Ile Arg Lys Met Glu Arg Glu Met Val Asp Thr Glu Thr Thr
                325                 330                 335

Ile Ser Ser Leu His Asn Ala Lys Thr Asn Tyr Met Leu Glu Ile Ser
            340                 345                 350

Lys Leu Gln Thr Glu Ala Glu Ala His Met Leu Leu Lys Asn Glu Arg
        355                 360                 365

Asp Ser Thr Ile Gln Asn Ile Phe Phe His Tyr Asn Leu Gly Asn Val
    370                 375                 380

Pro Ser Thr Pro Phe Ser Thr Glu Val Val Leu Asn Leu Thr Asn Arg
385                 390                 395                 400

Ile Lys Ser Arg Leu Gly Glu Leu Glu Met Asp Leu Leu Asp Lys Lys
                405                 410                 415

Lys Ser Asn Glu Thr Ala Leu Ser Thr Ala Trp Asp Cys Tyr Met Asp
            420                 425                 430

Ala Asn Asp Arg Trp Lys Ser Ile Glu Ala Gln Lys Arg Ala Lys Asp
        435                 440                 445

Glu Ile Lys Met Gly Ile Ser Lys Arg Ile Glu Glu Lys Glu Ile Glu
    450                 455                 460

Arg Asp Ser Phe Glu Phe Glu Ile Ser Thr Val Asp Val Lys Gln Thr
465                 470                 475                 480

Asp Glu Arg Glu Lys Gln Val Gln Val Glu Leu Glu Arg Lys Thr Lys
                485                 490                 495
```

Gln Asn Ser Glu Arg Gly Phe Glu Ser Lys Ile Glu Gln Lys Gln His
500 505 510

Glu Ile Tyr Ser Leu Glu His Lys Ile Lys Thr Leu Asn Arg Glu Arg
515 520 525

Asp Val Met Ala Gly Asp Ala Glu Asp Arg Leu Leu Thr Arg Ile Asp
530 535 540

Glu Cys Lys Asp Arg Ile Arg Gly Val Leu Lys Gly Arg Leu Pro Pro
545 550 555 560

Glu Lys Asp Met Lys Arg Glu Ile Val Gln Ala Leu Arg Ser Ile Glu
565 570 575

Arg Glu Tyr Asp Asp Leu Ser Leu Lys Ser Arg Glu Ala Glu Lys Glu
580 585 590

Val Asn Met Leu Gln Met Lys Ile Gln Glu Val Asn Asn Ser Leu Phe
595 600 605

Lys His Asn Lys Asp Thr Glu Ser Arg Lys Arg Tyr Ile Glu Ser Lys
610 615 620

Leu Gln Ala Leu Lys Gln Glu Ser Val Thr Ile Asp Ala Tyr Pro Lys
625 630 635 640

Leu Leu Glu Ser Ala Lys Asp Lys Arg Asp Asp Arg Lys Arg Glu Tyr
645 650 655

Asn Met Ala Asn Gly Met Arg Gln Met Phe Glu Pro Phe Glu Lys Arg
660 665 670

Ala Arg Gln Glu His Ser Cys Pro Cys Cys Glu Arg Ser Phe Thr Ala
675 680 685

Asp Glu Glu Ala Ser Phe Ile Lys Lys Gln Arg Val Lys Ala Ser Ser
690 695 700

Thr Gly Glu His Leu Lys Ala Leu Ala Val Glu Ser Ser Asn Ala Asp
705 710 715 720

Ser Val Phe Gln Gln Leu Asp Lys Leu Arg Ala Val Phe Glu Glu Tyr
725 730 735

Ser Lys Leu Thr Thr Glu Ile Ile Pro Leu Ala Glu Lys Thr Leu Gln
740 745 750

Glu His Thr Glu Glu Leu Gly Gln Lys Ser Glu Ala Leu Asp Asp Val
755 760 765

Leu Gly Ile Ser Ala Gln Ile Lys Ala Asp Lys Asp Ser Ile Glu Ala
770 775 780

Leu Val Gln Pro Leu Glu Asn Ala Asp Arg Ile Phe Gln Glu Ile Val
785 790 795 800

Ser Tyr Gln Lys Gln Ile Glu Asp Leu Glu Tyr Lys Leu Asp Phe Arg
805 810 815

Gly Leu Gly Val Lys Thr Met Glu Glu Ile Gln Ser Glu Leu Ser Ser
820 825 830

Leu Gln Ser Ser Lys Asp Lys Leu His Gly Glu Leu Glu Lys Leu Arg

```
        835                 840                 845

Asp Asp Gln Ile Tyr Met Glu Arg Asp Ile Ser Cys Leu Gln Ala Arg
    850                 855                 860

Trp His Ala Val Arg Glu Glu Lys Ala Lys Ala Ala Asn Leu Leu Arg
865                 870                 875                 880

Asp Val Thr Lys Ala Glu Glu Asp Leu Glu Arg Leu Ala Glu Glu Lys
                885                 890                 895

Ser Gln Leu Asp Leu Asp Val Lys Tyr Leu Thr Glu Ala Leu Gly Pro
            900                 905                 910

Leu Ser Lys Glu Lys Glu Gln Leu Leu Ser Asp Tyr Asn Asp Met Lys
        915                 920                 925

Ile Arg Arg Asn Gln Glu Tyr Glu Glu Leu Ala Glu Lys Lys Arg Asn
    930                 935                 940

Tyr Gln Gln Glu Val Glu Ala Leu Leu Lys Ala Ser Tyr Lys Ile Asn
945                 950                 955                 960

Asp Cys Phe Thr Arg Tyr His Asp Leu Lys Lys Gly Glu Arg Leu Asp
                965                 970                 975

Asp Ile Gln Glu Lys Gln Arg Leu Ser Asp Ser Gln Leu Gln Ser Cys
            980                 985                 990

Glu Ala Arg Lys Asn Glu Leu Ala Gly Glu Leu Asn Arg Asn Lys Asp
        995                1000                1005

Leu Met Arg Asn Gln Asp Gln Leu Arg Arg Asn Ile Glu Asp Asn Leu
   1010                1015                1020

Asn Tyr Arg Thr Thr Lys Ala Lys Val Glu Glu Leu Thr Arg Glu Ile
1025                1030                1035                1040

Glu Ser Leu Glu Glu Gln Ile Leu Asn Ile Gly Gly Ile Ala Ala Val
                1045                1050                1055

Glu Ala Glu Ile Val Lys Ile Leu Arg Glu Arg Glu Arg Leu Leu Ser
            1060                1065                1070

Glu Leu Asn Arg Cys Arg Gly Thr Val Ser Val Tyr Glu Ser Ser Ile
        1075                1080                1085

Ser Lys Asn Arg Val Glu Leu Lys Gln Ala Gln Tyr Lys Asp Ile Asp
   1090                1095                1100

Lys Arg His Phe Asp Gln Leu Ile Gln Leu Lys Thr Thr Glu Met Ala
1105                1110                1115                1120

Asn Lys Asp Leu Asp Arg Tyr Tyr Asn Ala Leu Asp Lys Ala Leu Met
                1125                1130                1135

Arg Phe His Thr Met Lys Met Glu Glu Ile Asn Lys Ile Ile Arg Glu
            1140                1145                1150

Leu Trp Gln Gln Thr Tyr Arg Gly Gln Asp Met Asp Tyr Ile Arg Ile
        1155                1160                1165

His Ser Asp Ser Glu Gly Ala Gly Thr Arg Ser Tyr Ser Tyr Lys Val
   1170                1175                1180
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Leu Met Gln Thr Gly Asp Thr Glu Leu Glu Met Arg Gly Arg Cys Ser
1185                1190                1195                1200

Ala Gly Gln Lys Val Leu Ala Ser Leu Ile Ile Arg Leu Ala Leu Ala
                1205                1210                1215

Glu Thr Phe Cys Leu Asn Cys Gly Ile Leu Ala Leu Asp Glu Pro Thr
            1220                1225                1230

Thr Asn Leu Asp Gly Pro Asn Ser Glu Ser Leu Ala Gly Ala Leu Leu
        1235                1240                1245

Arg Ile Met Glu Asp Arg Lys Gly Gln Glu Asn Phe Gln Leu Ile Val
    1250                1255                1260

Ile Thr His Asp Glu Arg Phe Ala Gln Met Ile Gly Gln Arg Gln His
1265                1270                1275                1280

Ala Glu Lys Tyr Tyr Arg Val Ala Lys Asp Asp Met
                1285                1290


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<211> 264
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> SITE
<222> (1)..(264)
<223> /note="XRCC4"

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Met Ile Gly Val Asp Ser Lys Ser Ser Ser Thr Thr Phe Ile Glu Thr
  1               5                  10                  15

Met Val Glu Ser Glu Lys Thr Lys His Thr Cys Leu Arg Leu Glu Ile
             20                  25                  30

Ser Gly Ala Asp Pro Ile Phe Val Lys Gly Thr Trp His Asn Ser Arg
         35                  40                  45

Phe Asp Ile Ser Val Thr Asp Gly Ser Ser Ser Trp Ile Cys Asn Ala
     50                  55                  60

Thr Glu Glu Glu Val Ala Glu Arg Ala Ala Gln Trp Asp Gln Pro Val
 65                  70                  75                  80

Ser Glu Tyr Leu Lys Leu Ala Glu Gln Tyr Leu Gly Phe Gln Gln Pro
                 85                  90                  95

Asn Ser Val Tyr Ser Phe Ser Asp Ala Leu Glu Gly Ser Lys Arg Leu
            100                 105                 110

Ser Trp Thr Phe Glu Lys Glu Gly Thr Lys Leu Glu Trp Arg Trp Lys
        115                 120                 125

Cys Lys Pro Ser Asp Asp Ser Lys Lys Ile Thr Val Gly Ile Leu Asp
    130                 135                 140

Phe Leu Met Glu Ala Asn Ile Arg Leu Ser Glu Glu Val Val Asn Lys
145                 150                 155                 160
```

```
Thr Arg Ser Phe Glu Lys Met Arg Ser Glu Ala Glu Arg Cys Leu Ala
                165                 170                 175

Gln Gly Glu Lys Leu Cys Asp Glu Lys Thr Glu Phe Glu Ser Ala Thr
            180                 185                 190

Tyr Ala Lys Phe Leu Ser Val Leu Asn Ala Lys Lys Ala Lys Leu Arg
        195                 200                 205

Ala Leu Arg Asp Lys Glu Asp Ser Val Arg Val Val Glu Glu Glu Glu
    210                 215                 220

Ser Thr Asp Lys Ala Glu Ser Phe Glu Ser Gly Arg Ser Asp Asp Glu
225                 230                 235                 240

Lys Ser Glu Glu Glu Ala Ser Lys Lys Ala Thr Ser Ser Lys Ala Arg
                245                 250                 255

Gly Gly Lys Arg Ala Ala Arg Ser
            260
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<210> 36
<211> 334
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)..(334)
<223> /note="XRCC4 homologue"

<400> 36

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Met Glu Arg Lys Ile Ser Arg Ile His Leu Val Ser Glu Pro Ser Ile
  1               5                  10                  15

Thr His Phe Leu Gln Val Ser Trp Glu Lys Thr Leu Glu Ser Gly Phe
             20                  25                  30

Val Ile Thr Leu Thr Asp Gly His Ser Ala Trp Thr Gly Thr Val Ser
         35                  40                  45

Glu Ser Glu Ile Ser Gln Glu Ala Asp Asp Met Ala Met Glu Lys Gly
     50                  55                  60

Lys Tyr Val Gly Glu Leu Arg Lys Ala Leu Leu Ser Gly Ala Gly Pro
 65                  70                  75                  80

Ala Asp Val Tyr Thr Phe Asn Phe Ser Lys Glu Ser Cys Tyr Phe Phe
                 85                  90                  95

Phe Glu Lys Asn Leu Lys Asp Val Ser Phe Arg Leu Gly Ser Phe Asn
            100                 105                 110

Leu Glu Lys Val Glu Asn Pro Ala Glu Val Ile Arg Glu Leu Ile Cys
        115                 120                 125

Tyr Cys Leu Asp Thr Ile Ala Glu Asn Gln Ala Lys Asn Glu His Leu
    130                 135                 140

Gln Lys Glu Asn Glu Arg Leu Leu Arg Asp Trp Asn Asp Val Gln Gly
145                 150                 155                 160

Arg Phe Glu Lys Cys Val Ser Ala Lys Glu Ala Leu Glu Thr Asp Leu
```

```
                165                 170                 175

Tyr Lys Arg Phe Ile Leu Val Leu Asn Glu Lys Lys Thr Lys Ile Arg
            180                 185                 190

Ser Leu His Asn Lys Leu Leu Asn Ala Ala Gln Glu Arg Glu Lys Asp
        195                 200                 205

Ile Lys Gln Glu Gly Glu Thr Ala Ile Cys Ser Glu Met Thr Ala Asp
    210                 215                 220

Arg Asp Pro Val Tyr Asp Glu Ser Thr Asp Glu Glu Ser Glu Asn Gln
225                 230                 235                 240

Thr Asp Leu Ser Gly Leu Ala Ser Ala Ala Val Ser Lys Asp Asp Ser
                245                 250                 255

Ile Ile Ser Ser Leu Asp Val Thr Asp Ile Ala Pro Ser Arg Lys Arg
            260                 265                 270

Arg Gln Arg Met Gln Arg Asn Leu Gly Thr Glu Pro Lys Met Ala Pro
        275                 280                 285

Gln Glu Asn Gln Leu Gln Glu Lys Glu Lys Pro Asp Ser Ser Leu Pro
    290                 295                 300

Glu Thr Ser Lys Lys Glu His Ile Ser Ala Glu Asn Met Ser Leu Glu
305                 310                 315                 320

Thr Leu Arg Asn Ser Ser Pro Glu Asp Leu Phe Asp Glu Ile
                325                 330
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<210> 37
<211> 421
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> SITE
<222> (1)..(421)
<223> /note="XRCC4 homologue"

<400> 37

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Met Ser Gln Leu Thr Glu Phe Ile Ser Cys Ile Pro Val Val Asn Glu
  1               5                  10                  15

Glu Gln Asn Glu Glu Asp Glu Arg Gly Leu Cys Lys Ile Gln Ile Glu
             20                  25                  30

Asp Gly Ala Met Leu Glu Thr Leu Asp Glu Asn Ser Leu Ser Gly Leu
         35                  40                  45

Arg Ile Glu Lys Met Leu Val Ser Glu Gly Thr Gly Ile Phe Ser Lys
     50                  55                  60

Ser Ser Phe Gly Ile Asn Asp Leu Arg Ile Phe Thr Gly Glu Asn Ile
 65                  70                  75                  80

Asp Glu Glu Ser Lys Lys Tyr Val Trp Tyr Glu Leu Leu Lys Met Leu
                 85                  90                  95

Thr Gly His Lys Val Tyr Ile Ala Ser Leu Asp Glu Lys Val Val Phe
            100                 105                 110
```

```
Thr Lys Trp Thr Cys Arg Met Gln Asp Asp Glu Val Trp Lys Val Val
        115                 120                 125

Met Glu Leu Glu Ser Ser Ala Ile Ile Arg Lys Ile Ala Glu Leu Thr
    130                 135                 140

Leu His Pro Val Lys Lys Gly Glu Ile Asp Leu Phe Glu Met Ala Asp
145                 150                 155                 160

Lys Leu Tyr Lys Asp Ile Cys Cys Val Asn Asp Ser Tyr Arg Asn Ile
                165                 170                 175

Lys Glu Ser Asp Ser Ser Asn Arg Asn Arg Val Glu Gln Leu Ala Arg
            180                 185                 190

Glu Arg Glu Leu Leu Asp Lys Leu Leu Glu Thr Arg Asp Glu Arg Thr
        195                 200                 205

Arg Ala Met Met Val Thr Leu Leu Asn Glu Lys Lys Lys Lys Ile Arg
    210                 215                 220

Glu Leu His Glu Ile Leu Arg Gln Asn Asn Ile Lys Leu Ser Asp Asp
225                 230                 235                 240

Asp Val Leu Asp Ser Ala Leu Ile Asn Thr Glu Val Gln Lys Pro Ile
                245                 250                 255

Ser Glu Leu Asn Ser Pro Gly Lys Arg Met Lys Arg Arg Lys Thr Val
            260                 265                 270

Val Glu Pro Gln Asn Leu Gln Lys Lys Leu Lys Asp Thr Ser Arg Arg
        275                 280                 285

Arg Ala Asn Arg Lys Ile Ser Asn Gln Ser Val Ile Lys Met Glu Asp
    290                 295                 300

Asp Asp Phe Asp Asp Phe Gln Phe Phe Gly Leu Ser Lys Arg Pro Ile
305                 310                 315                 320

Ile Thr Ala Lys Asp Lys Leu Ser Glu Lys Tyr Asp Asp Ile Thr Ser
                325                 330                 335

Phe Gly Asp Asp Thr Gln Ser Ile Ser Phe Glu Ser Asp Ser Ser Ser
            340                 345                 350

Asp Val Gln Lys His Leu Val Ser Leu Glu Asp Asn Gly Ile Gln Ile
        355                 360                 365

Ser Ala Gly Arg Ser Asp Glu Asp Tyr Gly Asp Ile Ser Gly Ser Glu
    370                 375                 380

Ser Glu Thr Asp Ala Ser Ala Gly Glu Lys Lys Ser Ser Asn His Ser
385                 390                 395                 400

Glu Gln Ser Gly Asn Asp Arg Glu Pro Cys Leu Gln Thr Glu Ser Glu
                405                 410                 415

Thr Asp Ile Glu Thr
            420
```